

Db 162 TREGNVT-STHSRNITQGEWSQKTYCQVTFKOPARKCSESDPRGVLSYLSP 220
 Qy 138 SPDLFLFRKSPTITCLVLDLAPSGBTNTLNSRASCKPVNHSRKKEKONGTLTVSTL 197
 Db 221 SPDLFLFRKSPTITCLVLDLAPSGBTNTLNSRASCKPVNHSRKKEKONGTLTVSTL 197
 Qy 198 PVGTRDWEGETYQCRYTHPHILPRAIMRSTTKLPGKRLAPVYMLPSPETGTR-TV 255
 Db 280 PVNINDWIEGETYQCRYTHPHILPDKDVRSLAKAPGKRAAPPDVYLFLPESEOGTKRVT 339
 Qy 256 TCLIRGYPSEISQWLFNNEEDHTGHHTTRPKOHGTPSPFLYSLVNSLWKG 315
 Db 340 TCLIQNFPADISQWLRNDSPQDQTTGPHKVSGSRPAFFSRSLVRSVWQKN 399
 Qy 316 LVCIRVWHEALPOSRTLEKSLHYSAG 341
 Db 400 KFTCQVWHEALSGSRILQKQWVKSTPG 425

RESULT 2
 PCT-US95-13795-2
 ; Sequence 2, Application PC/TUS9513795
 ; GENERAL INFORMATION:
 ; APPLICANT: HOLLIS, GREGORY F.
 ; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CHRISTINE E. CARTY
 ; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
 ; CITY: RAILWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07065-0307
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13795
 ; FILING DATE:
 ; NAME: CARTY, CHRISTINE E.
 ; REGISTRATION NUMBER: 36,099
 ; ATTORNEY/AGENT INFORMATION:
 ; REFERENCE/DOCKET NUMBER: 19911Y
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 594-6734
 ; TELEFAX: (908) 594-4720
 ; INFORMATION FOR SBO ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 426 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-13795-2
 ; Query Match 53.3%; Score 989; DB 5; Length 426;
 ; Best Local Similarity 56.7%; Pred. No. 1e-87; Indels 4; Gaps 3;
 ; Matches 185; Conservative 53; Mismatches 84; Index 4;
 ; Qy 18 VTIIPPTVLFSSCDPRGDAHSTICLICVSGPSPAKUHMLVQBARNLPEPYTRP 77
 ; Db 226 SPDLFLFRKSPTITCLVLDLAPSGBTNTLNSRASCKPVNHSRKKEKONGTLTVSTL 284
 ; Qy 78 KRGQQFSLOSEVNITQGQMSNTYTCVHKGNSFEDSSRKCADSNRGVSYLSRP 137
 ; Db 107 MNFIPPTVLFSSCDPRGDAHSTICLICVSGPSPAKUHMLVQBARNLPEPYTRP 77
 ; Db 157 KQGKVY-STHSRNITQGEWSQKTYCQVTFKOPARKCSESDPRGVLSYLSP 225
 ; Qy 138 SPDLFLFRKSPTITCLVLDLAPSGBTNTLNSRASCKPVNHSRKKEKONGTLTVSTL 197
 ; Db 226 SPDLFLFRKSPTITCLVLDLAPSGBTNTLNSRASCKPVNHSRKKEKONGTLTVSTL 284
 ; Qy 198 PVGTRDWEGETYQCRYTHPHILPRAIMRSTTKLPGKRLAPVYMLPSPETGTR-TV 255
 ; Db 285 PVADATDWEGETYQCRYTHPHILPDKDVRSLAKAPGKRAAPPDVYLFLPESEOGTKRVT 339
 ; Qy 256 TCLIRGYPSEISQWLFNNEEDHTGHHTTRPKOHGTPSPFLYSLVNSLWKG 315
 ; Db 340 TCLIQNFPADISQWLRNDSPQDQTTGPHKVSGSRPAFFSRSLVRSVWQKN 399
 ; Qy 316 LVCIRVWHEALPOSRTLEKSLHYSAG 341
 ; Db 400 KFTCQVWHEALSGSRILQKQWVKSTPG 425

RESULT 3
 US-09-479-614-14
 ; Sequence 14, Application US/09479614
 ; Patent No. 657372
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine
 ; APPLICANT: Weber, Eric
 ; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
 ; FILE REFERENCE: P-1047
 ; CURRENT APPLICATION NUMBER: US/09/479, 614
 ; CURRENT FILING DATE: 2000-01-07
 ; EARLIER APPLICATION NUMBER: 60/115, 033
 ; EARLIER FILING DATE: 1999-01-07
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Felis catus
 ; US-09-479-614-14
 ; Query Match 52.4%; Score 972; DB 4; Length 431;
 ; Best Local Similarity 56.7%; Pred. No. 4.7e-86;
 ; Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;
 ; Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;
 ; Qy 18 VTIIPPTVLFSSCDPRGDAHSTICLICVSGPSPAKUHMLVQBARNLPEPYTRP 77
 ; Db 107 MNFIPPTVLFSSCDPRGDAHSTICLICVSGPSPAKUHMLVQBARNLPEPYTRP 77
 ; Db 157 KQGKVY-STHSRNITQGEWSQKTYCQVTFKOPARKCSESDPRGVLSYLSP 225
 ; Qy 138 SPDLFLFRKSPTITCLVLDLAPSGBTNTLNSRASCKPVNHSRKKEKONGTLTVSTL 197
 ; Db 226 SPDLFLFRKSPTITCLVLDLAPSGBTNTLNSRASCKPVNHSRKKEKONGTLTVSTL 284
 ; Qy 198 PVGTRDWEGETYQCRYTHPHILPRAIMRSTTKLPGKRLAPVYMLPSPETGTR-TV 255
 ; Db 285 PVADATDWEGETYQCRYTHPHILPDKDVRSLAKAPGKRAAPPDVYLFLPESEOGTKRVT 339
 ; Qy 256 TCLIRGYPSEISQWLFNNEEDHTGHHTTRPKOHGTPSPFLYSLVNSLWKG 315
 ; Db 340 TCLIQNFPADISQWLRNDSPQDQTTGPHKVSGSRPAFFSRSLVRSVWQKN 399
 ; Qy 316 LVCIRVWHEALPOSRTLEKSLHYSAG 341
 ; Db 400 KFTCQVWHEALSGSRILQKQWVKSTPG 425

RESULT 4
 US-09-479-614-2
 ; Sequence 2, Application US/09479614
 ; Patent No. 657372
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine
 ; APPLICANT: Weber, Eric

RESULT 5
 US-09-479-614-29
 ; Sequence 29: Application US/09479614
 ; Patent No. 6573372
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine
 ; APPLICANT: Weber, Eric
 ; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
 ; FILE REFERENCE: P-1047
 ; CURRENT APPLICATION NUMBER: US/09/479,614
 ; CURRENT FILING DATE: 2000-01-07
 ; EARLIER APPLICATION NUMBER: 60/115,033
 ; EARLIER FILING DATE: 1999-01-07
 ; NUMBER OF SEQ ID NOS: 34
 ; SEQ ID NO 2 :
 ; LENGTH: 496
 ; TYPE: PRT; Organism: *Felis catus*
 ; US-09-479-614-2

Query Match 52.4%; Score 972; DB 4; Length 496;
 Best Local Similarity 55.7%; Pred. No. 5; 8e-86;
 Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;

Db 232 KQEGKVTT-STHSLBNITQGEWBSQKTTQGFTFEDHARKTCSDPGVSTLSSPP 290
 Qy 138 SPPLFLIKSPPTTCLVYDЛАSSKGTTNTLMSRASGCPVNISTRKKEKQKGTLTSTL 197
 Db 291 SPUDLVHVKSPKTCIYLVDLANTDGM-LTWSRENJSVHPDPMVKKQYQNTITVSTL 349
 Qy 198 PVRGRDWRGETYQCRVTHPHLPRALMESTTKLPGKELAPETM-LEPSPB-ETGTTTV 255
 Db 350 PVDATDWAEGETYQCKVTHPDPKDTTRIAKAPGRFPPPTVVPDPGEGKTKRVL 409
 Qy 256 TCLIRGFYFSEISVQMLENEEDHTGHTTRPQKDGTDSFPLYSLVMSLPIEKG 315
 Db 410 TCLIQNFFPDPDISVQMLNDSPVTRQATTPHKAQGSPAPFVSRLEVSRADWEQRD 469
 Qy 316 LVCRCVHIALPSRTLEKSLHYSAG 341
 Db 470 VFTCQVHIALPGRTRKKSYSKPG 495

RESULT 6
 US-09-192-545-2
 ; Sequence 2: Application US/09192545
 ; Patent No. 6118044
 ; GENERAL INFORMATION:
 ; APPLICANT: Karasuyama, Hajime
 ; APPLICANT: Tava, Choji
 ; APPLICANT: Matsumoto, Kunie
 ; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
 ; FILE REFERENCE: 79979570
 ; CURRENT APPLICATION NUMBER: US/09/192,545
 ; CURRENT FILING DATE: 1998-11-13
 ; EARLIER APPLICATION NUMBER: JP H09 9-313989
 ; EARLIER FILING DATE: 1997-11-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2 :
 ; LENGTH: 561
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: Description of Artificial Sequence: Designed heavy
 ; US-09-192-545-2

Query Match 36.3%; Score 673; DB 3; Length 561;
 Best Local Similarity 41.8%; Pred. No. 8.1e-57;
 Matches 147; Conservative 53; Mismatches 133; Indels 20; Gaps 7;

Db 211 FTCVHTTIPPSFNESTRLVPT--HSLSPPWPSYIHRDPNA-FHSTIOLYCPIGH 265
 Qy 52 SPAKVHTWLVDQGEARNLFPYTRTRREGQTSFSTQSEVNTIQGOMMSNTYTCVHN 111
 Db 266 ILNDVSYWMLDRETTIATQVTLIKE GKLASICKSKNITEQWMSSESTPCTVTSQ 324
 Qy 112 GSFEDESRKCADSNPREGVASYLRSRSPDFTIREKSTPITCIVDLPASKGTVNLTWSRA 171
 Db 325 GVDYLAKTRCPDHEPREGATVLISSPLDLYQNGAKPKLTLVVDLESK-NVNTWNB 383
 Qy 172 SGKPVNSTRKEEKORGTLTWTSLPVGTRDWSGETYQCRVTHPHLPRALMSTTKL 231
 Db 384 KKTTSVSAQWYTRHHNATTSILPVAQDWIGGYQCVVDRDPKPKIVRSIT-LP 442
 Qy 232 -GKRLAIPPEVYMLPSPBEGTTRTCTLRGFYFSEISVQMLFNEEDHTGHTTRPQ 289
 Db 443 QVSQSAPEVYVFPBPBEESEDKRTLCLIONFPFDVSDQVLDGKLTNSQHSTP 502
 Qy 290 KONGTDPFPLYSRMSVWKSWEKGWLTQCRVHIALPSRTLEKSLHYSAG 342
 Db 503 KENGNSQCPFRPSLRSVAKTLWTKOPTCQVTHAIKQKRLKEMTSIGN 555
 Qy 78 KREGGQTFSTQSEWVNTQGQMSNTYTCVHNGSIFEDSSRKADSNSRGVSAVLSRP 137

NUMBER OF SEQUENCES: 60
 COMPUTER: IBM PC compatible
 COMPUTER READABLE FORM: OPERATING SYSTEM: PC-DOS/MS-DOS
 CORRESPONDENCE ADDRESS: SOFTWARE: PatentIn Release #1.0, Version #1.30
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,981
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/178583
 FILING DATE: 07-JAN-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,539D
 FILING DATE: 21-APR-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET NUMBER: P0718P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 TELEFAX: 650/552-9881
 INFORMATION FOR SEQ ID NO: 54:
 LENGTH: 106 amino acids
 SOURCE/CHARACTERISTICS:
 TYPE: Amino Acid
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 US-08-646-981-16
 Query Match 29.0%: Score 538; DB 2; Length 106;
 Best Local Similarity 98.1%; Pred. No. 8 9e-45; Mismatches 0; Indels 0; Gaps 0;
 Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 129 GVSAYLSRSPSPFLFIRKSPPTICLVVLDLASSKGTVNLTWASRASGVNHS
 1 GVSAYLSRSPSPFLFIRKSPPTICLVVLDLASSKGTVNLTWASRASGVNHS
 188 KRN 60
 189 GFLTYVTSILPGVIRDWEGETQCRVPHPLRALKMSTIKPG 232
 61 GFLTYVTSILPGVIRDWEGETQCRVPHPLRALKMSTIKPG 104
 RESULT 11
 US-08-646-981-16
 Sequence 16, Application US/08646981
 Patent No. 582183
 GENERAL INFORMATION:
 APPLICANT: MAEDA, HIROAKI
 APPLICANT: EDA, YASUO
 APPLICANT: KIMACHI, KAZUHIKO
 APPLICANT: ONO, YOICHI
 APPLICANT: TOKIYOSHI, SACHIO
 TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
 TITLE OF INVENTION: IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 STREET: PO BOX 747
 CITY: FALLS CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/164,025A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 530
 Query Match 27.6%: Score 512; DB 2; Length 334;
 Best Local Similarity 35.9%; Pred. No. 1.7e-41; Mismatches 60; Indels 38; Gaps 12;
 Matches 123; Conservative 60; Mismatches 122; Indels 38; Gaps 12;
 23 PTYVLFHSSCDPGRDAHSITQQLICLVSQSFPAKHWVMT--LVDGQAENLPPYTRPK 78
 5 PSVFLDPSQG--STSGSIVVALCIVSGYPPETVSWNSLTSG-----VHTPSD 55
 79 REGGQFQSIQSEWNTIOTGOMMSNTYCHVKG-----NGSIFE--DSSRK 121
 56 LQSSGLYSLSSMMVTPSPSRW-SSETPTCNAVAPASKITKUDVKVPRKENGIVPRPPDKC 114
 122 CADSNPRGYSAYLSRSPSPFLFIRKSPPTICLVVLDLASSKGTVNLTWASRASGVNHS- 179
 94 115 PAPMLGGSVFVPPKFKDTIILAKRPEVTCVWVLDQGDPEPDEVQISWP-VDGKQHQTAK 173
 180 TRKEEKQRGQTLTWSTLPGVGDWIGETQCRVPHPLRALKMSTIKPGKRAPEV 239
 174 TQPPEBFQFENGTYRVSVLPIGHQDWLRKQFTCKVNNKALPSPIERNTISKARGQAHQPSV 233
 240 YMLPSPSPER-TGTRTRVCLINGFYPPEBISQWLFNNEEDHTGHTTRPKDQHGDPSF 298
 234 YVLPSPRBSLISKVNLCLIKOFPDPDIDVWQSHQSQEPEKSQYRTPPQDLE-DGSY 291
 299 FLYSRMLVNSKINVEKGNAVLTCRVHEALPGSRTELESLHYSG 341
 292 FLYSLVTSVKSRSQRGDPTICATMEALHNRT-QSLSHSBPG 333
 RESULT 12
 US-08-444-025A-1
 Sequence 1, Application US/08464025A
 Patent No. 5994514
 GENERAL INFORMATION:
 APPLICANT: Jardieu et al.
 TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/164,025A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET NUMBER: P0718C3

TELECOMMUNICATION INFORMATION:
 TELEFAX: 650/9225-489

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids

TYPE: Amino Acid
 TOPOLOGY: Linear

; US 08-464-023A-1

Query Match

Similarity

Score

DB

2

Length

119

Indels

8

Gaps

4

Best Local

Similarity

88.9%

Pred.

No.

8.7e-42

1;

Mismatches

4;

Indels

8;

Gaps

4;

Matches

164;

Conservative

1;

Indels

8;

Gaps

4;

Best Local

Similarity

36.3%

Pred.

No.

1.7e-40

2;

Length

331;

Indels

27;

Gaps

12;

Matches

122;

Conservative

62;

Mismatches

125;

Indels

27;

Gaps

12;

US-08-464-023A-1

Query Match

Similarity

27.0%

Score

501.5;

DB

2;

Length

331;

Indels

27;

Gaps

11;

Matches

122;

Conservative

62;

Mismatches

125;

Indels

27;

Gaps

12;

US-08-464-023A-1

Query Match

Similarity

27.4%

Score

508;

DB

2;

Length

119;

Indels

8;

Gaps

4;

Matches

164;

Conservative

1;

Mismatches

4;

Indels

8;

Gaps

4;

Best Local

Similarity

88.9%

Pred.

No.

8.7e-42

1;

Mismatches

4;

Indels

8;

Gaps

4;

Matches

124;

Conservative

61;

Mismatches

125;

Indels

27;

Gaps

12;

US-08-464-023A-1

Query Match

Similarity

27.4%

Score

508;

DB

2;

Length

119;

Indels

8;

Gaps

4;

Matches

124;

Conservative

61;

Mismatches

125;

Indels

27;

Gaps

12;

US-08-464-023A-1

Query Match

Similarity

27.4%

Score

508;

DB

2;

Length

119;

Indels

8;

Gaps

4;

Matches

124;

Conservative

61;

Mismatches

125;

Indels

27;

Gaps

12;

US-08-464-023A-1

Query Match

Similarity

27.4%

Score

508;

DB

2;

Length

119;

Indels

8;

Gaps

4;

Matches

124;

Conservative

61;

Mismatches

125;

Indels

27;

Gaps

12;

US-08-464-023A-1

Query Match

Similarity

27.4%

Score

508;

DB

2;

Length

119;

Indels

8;

Gaps

4;

Matches

124;

Conservative

61;

Mismatches

125;

Indels

27;

Gaps

12;

US-08-464-023A-1

Query Match

Similarity

27.4%

Score

508;

DB

2;

Length

119;

Indels

8;

Gaps

4;

Matches

124;

Conservative

61;

Mismatches

125;

Indels

27;

Gaps

12;

US-08-464-023A-1

Query Match

Similarity

27.4%

Score

508;

DB

2;

Length

119;

Indels

8;

Gaps

4;

Matches

124;

Conservative

61;

Mismatches

125;

Indels

27;

Gaps

12;

US-08-464-023A-1

Query Match

Similarity

27.4%

Score

508;

DB

2;

Length

119;

Indels

8;

Gaps

4;

Matches

124;

Conservative

61;

Mismatches

125;

Indels

Db 140 RSTSESTAAIGCLVKDYFPEPVTVWSNSGALTSG--VHTPPAVL---QSSGLYSLSSV 192
 Qy 91 VAITQGOMSSNTYTCVKKH--NGSFEDSSRKCADSNP-----RGVAYLSRSPF 140
 Db 193 VVTTSSNF-GTQTYTCVNDHKPSNTKDVTKTVERKCCVECPCCPAPPVAGPSVFLPPK 251
 Qy 141 D-LFIRKSPPTICLVLAPSKGTVNLTWSRASGKCVNHSRKEEKORNGTITVSTLPV 199
 Db 252 DTIMISRPEVTCVWVVDVSHEDPEVOPNWYVTDGMEVNATKPRSBDFNSPFRVSVLT 311
 Qy 200 GTRDWFIEGETYQCRVTHPLPRAALMSTKPGKRLAPEVMLPSPPE-TGTRIVTCL 258
 Db 312 VHODWLNGKEYKCKVSKNGKLPAPIEKITSKTKGQPREPOVTLPPSRERMTKNVSLCL 371
 Qy 259 IRGFYPSBISVOMLFNNEBDHGHTTRPKDGHGDPSPFTLYSRMLVNTSIWEKGNLVT 318
 Db 372 VKGFPYPSDIAVENSGOPEN--NYKTPPMUD--SDGSFFLYSKLTVDKSRMGGNVS 427
 Qy 319 CRVHEALPGRSLTEKSLHYSAG 341
 Db 428 CSTMHEALHNYT-QKSLSLPG 449

Db 159 RSTSESTAAIGCLVKDYFPEPVTVWSNSGALTSG--VHTPPAVL---QSSGLYSLSSV 211
 Qy 91 VAITQGOMSSNTYTCVKKH--NGSFEDSSRKCADSNP-----RGVAYLSRSPF 140
 Db 212 VVTTSSNF-GTQTYTCVNDHKPSNTKDVTKTVERKCCVECPCCPAPPVAGPSVFLPPK 270
 Qy 141 D-LFIRKSPPTICLVLAPSKGTVNLTWSRASGKCVNHSRKEEKORNGTITVSTLPV 199
 Db 271 DTIMISRPEVTCVWVVDVSHEDPEVOPNWYVTDGMEVNATKPRSBDFNSPFRVSVLT 330
 Qy 200 GTRDWFIEGETYQCRVTHPLPRAALMSTKPGKRLAPEVMLPSPPE-TGTRIVTCL 258
 Db 331 VHODWLNGKEYKCKVSKNGKLPAPIEKITSKTKGQPREPOVTLPPSRERMTKNVSLCL 390
 Qy 259 IRGFYPSBISVOMLFNNEBDHGHTTRPKDGHGDPSPFTLYSRMLVNTSIWEKGNLVT 318
 Db 391 VKGFPYPSDIAVENSGOPEN--NYKTPPMUD--SDGSFFLYSKLTVDKSRMGGNVS 446
 Qy 319 CRVHEALPGRSLTEKSLHYSAG 341
 Db 447 CSTMHEALHNYT-QKSLSLPG 468

RESULT 15

US-07-934-373C-23

; Sequence 23, Application US/07934373C
 ; Patent No. 5821337

; GENERAL INFORMATION:

APPLICANT: Paul J. Carter

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/934,373C

FILING DATE: 21-AUG-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/115272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 469 amino acids

TYPE: Amino Acid

TAXONOMY: Linear

US-07-934-373C-23

Search completed: February 26, 2004, 12:04:43
 Job time : 25 secs

Query Match 26.5%; Score 492.5; DB 2; Length 469;
 Best Local Similarity 36.5%; Pred. No. 2.2e-39;
 Matches 118; Conservative 57; Mismatches 119; Indels 29; Gaps 11;

Qy 35 RDAHSTIQOLCLVNSGRSPAKVHTW---LVDGQBAENLPPYTRPKREGGQTPSLOSE 90

OM protein - protein search, using sw model
 Run on: February 26, 2004, 11:59:57 ; search time 39 seconds
 (without alignments)
 1900.379 Million cell updates/sec

Title: US-09-401-636-8
 Perfect score: 1856
 Sequence: 1 BFMHHHHHMLSLPESGPVLT.HEALPGSRITLEKSLHYSAGN 342

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pupbaa/US07_PUBCOMB.pep: *
 2: /cgn2_6/ptodata/2/pupbaa/PCM_NEW_PUB.pep: *
 3: /cgn2_6/ptodata/2/pupbaa/US06_NEW_PUB.pep: *
 4: /cgn2_6/ptodata/2/pupbaa/US06_PUBCOMB.pep: *
 5: /cgn2_6/ptodata/2/pupbaa/US07_NEW_PUB.pep: *
 6: /cgn2_6/ptodata/2/pupbaa/PCRS_PUBCOMB.pep: *
 7: /cgn2_6/ptodata/2/pupbaa/US08_NEW_PUB.pep: *
 8: /cgn2_6/ptodata/2/pupbaa/US08_PUBCOMB.pep: *
 9: /cgn2_6/ptodata/2/pupbaa/US09_B_PUBCOMB.pep: *
 11: /cgn2_6/ptodata/2/pupbaa/US09_C_PUBCOMB.pep: *
 12: /cgn2_6/ptodata/2/pupbaa/US09_NEW_PUB.pep: *
 13: /cgn2_6/ptodata/2/pupbaa/US10_A_PUBCOMB.pep: *
 14: /cgn2_6/ptodata/2/pupbaa/US10_B_PUBCOMB.pep: *
 15: /cgn2_6/ptodata/2/pupbaa/US10_C_PUBCOMB.pep: *
 16: /cgn2_6/ptodata/2/pupbaa/US10_NEW_PUB.pep: *
 17: /cgn2_6/ptodata/2/pupbaa/US66_NEW_PUB.pep: *
 18: /cgn2_6/ptodata/2/pupbaa/US66_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	1856	100.0	342	9 US-09-401-636-8
2	1856	100.0	342	14 US-09-176-664-8
3	1844.5	88.6	341	9 US-09-401-636-11
4	1844.5	88.6	341	14 US-10-176-664-11
5	1847.5	85.5	341	9 US-09-401-636-3
6	1587.5	85.5	341	14 US-10-176-664-3
7	1887.5	85.5	345	9 US-09-401-636-10
8	1887.5	85.5	345	14 US-10-176-664-10
9	1688.5	84.5	341	9 US-09-401-636-9
10	1688.5	84.5	341	14 US-10-176-664-9
11	1533.5	83.7	341	9 US-09-401-636-4
12	1533.5	83.7	341	14 US-10-176-664-4
13	1288.5	82.4	341	9 US-09-401-636-6
14	1288.5	82.4	341	14 US-10-176-664-6
15	1523.5	82.1	446	14 US-10-214-524-32

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Sequence description					
Sequence	Match	Score	DB	Length	Start
Sequence 8, Appli	100.0%	1856	9	342	
Sequence 8, Appli	Best local similarity	100.0%	Pred. No.	1	4e-146
Sequence 11, Appli	Matches	342;	Conservative	0;	Mismatches 0;
Sequence 11, Appli					Indels 0;
Sequence 3, Appli	QY				
Sequence 3, Appli	Db				
Sequence 10, Appli	1	EFHHHHHHHTLSPSGPVVIIIPPKVLFHSSCDPRGDAHSTIQLCLYSGFSPAKM			
Sequence 10, Appli	1	EFHHHHHHHTLSPSGPVVIIIPPKVLFHSSCDPRGDAHSTIQLCLYSGFSPAKM			
Sequence 9, Appli	QY				
Sequence 9, Appli	61	IVDGOBAENLFPYTRPKREGQFTSLSOSEVNITQGQMSNTTCHYRNGSTFF			
Sequence 4, Appli	Db				
Sequence 4, Appli	61	LVDQDQEAEMLFPYTRPKREGQFTSLSOSEVNITQGQMSNTTCHYRNGSTFF			
Sequence 6, Appli	QY				
Sequence 6, Appli	121	KCADSNPRGVSAVLSRSPSPFDLIRKSPITCIVDLDAPSKGTVNLWSRASCKP			
Sequence 32, Appli	Db				
Sequence 32, Appli	121	KCADSNPRGVSAVLSRSPSPFDLIRKSPITCIVDLDAPSKGTVNLWSRASCKP			

Sequence 5, Appli
Sequence 5, Appli
Sequence 36, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 29, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 329, App
Sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 60, Appli
Sequence 45, Appli
Sequence 37, Appli
Sequence 176, App
Sequence 176, App
Sequence 334, App
Sequence 10, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 26, Appli
Sequence 13, Appli
Sequence 28, Appli
Sequence 25, Appli

QY 181 RKEEKQRNGILTVTSLPGTRDMEGETIQCRVTHPLPRLMRSTKLPGKRLAPEVY 240 ; FILE REFERENCE: 10223/006001
 Db 181 RKEEKQRNGILTVTSLPGTRDMEGETIQCRVTHPLPRLMRSTKLPGKRLAPEVY 240 ; CURRENT APPLICATION NUMBER: US/09/401,636
 QY 241 MLPPSPEEGTTRTVCILRGFYSEISQWLFNEEDHTGHITTRPQKHDGTDPSFPL 300 ; CURRENT FILING DATE: 1999-09-22
 Db 241 MLPPSPEEGTTRTVCILRGFYSEISQWLFNEEDHTGHITTRPQKHDGTDPSFPL 300 ; PRIOR APPLICATION NUMBER: US 60/106,652
 QY 301 YSRMLVNLKSIWEKGNLVTCRVWHEALPSRTLKSLSYAGN 342 ; PRIOR FILING DATE: 1998-11-02
 Db 301 YSRMLVNLKSIWEKGNLVTCRVWHEALPSRTLKSLSYAGN 342 ; NUMBER OF SEQ ID NOS: 11
 ; SEQ ID NO: 11 ; SOFTWARE: FastaSeq for Windows Version 4.0
 ; LENGTH: 341 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetically generated proteins

RESULT 2
 US-10-176-664-8
 ; Sequence 8, Application US/10176664
 ; Publication No. US20030031663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hellman, Lars T.
 ; TITLE OF INVENTION: ENHANCED VACCINES
 ; FILE REFERENCE: 10223/006001
 ; CURRENT APPLICATION NUMBER: US/10/176,664
 ; CURRENT FILING DATE: 2002-06-19
 ; PRIOR APPLICATION NUMBER: US/09/401,636
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: US 60/106,652
 ; PRIOR FILING DATE: 1998-11-02
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastaSeq for Windows Version 4.0
 ; SEQ ID NO: 8
 ; LENGTH: 342
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetically generated proteins

Query Match 100.0%; Score 1856; DB 14; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.4e-146;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPHHHHHHTLSLPSGGPVITIPPTVKLHSSCDPRGAHSTIQLCLVSGESPAKVTW 60 ; Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;
 Db 1 EPHHHHHHTLSLPSGGPVITIPPTVKLHSSCDPRGAHSTIQLCLVSGESPAKVTW 60 ;
 ;
 QY 61 LVDGQAENLPPYTRPRBGGQFPLSSEVNITOGOMSNVYTCVKHNSIPFESSR 120 ;
 Db 61 LVDGQAENLPPYTRPRBGGQFPLSSEVNITOGOMSNVYTCVKHNSIPFESSR 120 ;
 ;
 QY 121 KCADSNPRGVSAYLSPSPDLPKRSPTITCLVDAPLSKVNLWMSRASGPVHST 180 ;
 Db 121 KCADSNPRGVSAYLSPSPDLPKRSPTITCLVDAPLSKVNLWMSRASGPVHST 180 ;
 ;
 QY 121 KCSSDPRTVSLSPSGLDVLVKAFKTCILVDAATMEG-MNLTWRSKEPPNGP 179 ;
 Db 121 KCSSDPRTVSLSPSGLDVLVKAFKTCILVDAATMEG-MNLTWRSKEPPNGP 179 ;
 ;
 QY 181 RKEEKQRNGILTVTSLPGTRDMEGETIQCRVTHPLPRLMRSTKLPGKRLAPEVY 240 ;
 Db 181 RKEEKQRNGILTVTSLPGTRDMEGETIQCRVTHPLPRLMRSTKLPGKRLAPEVY 240 ;
 ;
 QY 241 MLPPSPEEGTTRTVCILRGFYSEISQWLFNEEDHTGHITTRPQKHDGTDPSFPL 300 ;
 Db 241 MLPPSPEEGTTRTVCILRGFYSEISQWLFNEEDHTGHITTRPQKHDGTDPSFPL 300 ;
 ;
 QY 301 YSRMLVNLKSIWEKGNLVTCRVWHEALPSRTLKSLSYAGN 342 ;
 Db 301 YSRMLVNLKSIWEKGNLVTCRVWHEALPSRTLKSLSYAGN 342 ;
 ;
 RESULT 4
 US-10-176-664-11
 ; Sequence 11, Application US/10176664
 ; Publication No. US20030031663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hellman, Lars T.
 ; TITLE OF INVENTION: ENHANCED VACCINES
 ; FILE REFERENCE: 10223/006001
 ; CURRENT APPLICATION NUMBER: US/10/176,664
 ; CURRENT FILING DATE: 2002-06-19
 ; PRIOR APPLICATION NUMBER: US/09/401,636
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: US 60/106,652
 ; PRIOR FILING DATE: 1998-11-02
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastaSeq for Windows Version 4.0
 ; SEQ ID NO: 11
 ; LENGTH: 341
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetically generated proteins

Query Match 88.6%; Score 1644.5; DB 14; Length 341;
 Best Local Similarity 88.0%; Pred. No. 5.2e-129;
 Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;
 QY 1 EPHHHHHHTLSLPSGGPVITIPPTVKLHSSCDPRGAHSTIQLCLVSGESPAKVTW 60 ;

RESULT 3
 US-09-401-636-11
 ; Sequence 11, Application US/09401636
 ; Patient No. US20010038843A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hellman, Lars T.
 ; TITLE OF INVENTION: ENHANCED VACCINES

FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-10

Query Match1 Best Local Similarity 84.7%; Pred. No. 3.5e-14; Mismatches 23; Indels 17; Gaps 4;
Matches 298; Conservative 14; MisMatches 23; Indels 17; Gaps 4;

QY 1 EPHHHHHHTLSLPSGPGVTTIPPTVKLHS SCOPRGDAHSTIQLCIVSGSGSPAKHVTW 60
Db 1 EPHHHHHHTLSLPSGPGVTTIPPTVKLHS SCOPRGDAHSTIQLCIVSGSGSPAKHVTW 60

QY 61 LVDGQEAENLFPYTRPREGGOTFSILOSEVNTIQGQMMSSNTYTCVKHNGSIEFDSR 120
Db 61 LVDGQEAENLFPYTRPREGGOTFSILOSEVNTIQGQMMSSNTYTCVKHNGSIEFDSR 120

QY 121 KC-ADSNPPGVSAVLSPSPFDLPIRKSPFTIQLCIVSGSGSPAKHVTW 60
Db 121 KC-ADSNPPGVSAVLSPSPFDLPIRKSPFTIQLCIVSGSGSPAKHVTW 60

QY 122 RCTAESEPERGVASATLSPSPFDLPIRKSPFTIQLCIVSGSGSPAKHVTW 120
Db 122 RCTAESEPERGVASATLSPSPFDLPIRKSPFTIQLCIVSGSGSPAKHVTW 120

QY 173 --GKPVNHTSTRKEEKQRNGTTLVSTLPGTRDIEGTYQCRVTHPLPMLRSTTK 230
Db 173 --GKPVNHTSTRKEEKQRNGTTLVSTLPGTRDIEGTYQCRVTHPLPMLRSTTK 230

QY 180 PPGSPV----IKPQFNGTTSATLSPVNLNWSIWEKGNTYCRVWHEALGSRTLEKSLHYSAGN 342
Db 180 PPGSPV----IKPQFNGTTSATLSPVNLNWSIWEKGNTYCRVWHEALGSRTLEKSLHYSAGN 342

QY 231 PGKELAPEVYMLRSPSPETGTRTIVTILRGYPSESVQMLFNNEDHTGHTRRQK 293
Db 231 PGKELAPEVYMLRSPSPETGTRTIVTILRGYPSESVQMLFNNEDHTGHTRRQK 293

QY 291 DHGTDPSFLYSLVNLWSIWEKGNTYCRVWHEALGSRTLEKSLHYSAGN 342
Db 291 DHGTDPSFLYSLVNLWSIWEKGNTYCRVWHEALGSRTLEKSLHYSAGN 342

QY 294 DHGTDPSFLYSLVNLWSIWEKGNTYCRVWHEALGSRTLEKSLHYSAGN 345
Db 294 DHGTDPSFLYSLVNLWSIWEKGNTYCRVWHEALGSRTLEKSLHYSAGN 345

RESULT 8
US-10-176-664-10

; Sequence 10, Application US-10-176664
; Publication No. US20030031663A1

; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636

; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US/10/176,664

; PRIOR FILING DATE: 2002-06-19
; FILE REFERENCE: 10223/006001
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US/10/176,664

; NUMBER OF SEQ ID NOS: 11
; NUMBER OF SEQ ID NOS: 11
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RESULT 9
US-09-401-636-9

; Sequence 9, Application US/09401636
; Publication No. US20010038843A1

; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636

; CURRENT FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
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RESULT 10
US-10-176-664-9

; Sequence 9, Application US/10176664
; Publication No. US20030031663A1

; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664

CURRENT FILING DATE: 2002-06-19
 PRIORITY APPLICATION NUMBER: US/09/401,636
 PRIOR FILING DATE: 1999-09-22
 NUMBER OF SEQ ID NOS: 11
 PRIORITY APPLICATION NUMBER: US 60/106,652
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 9
 LENGTH: 341
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE: OTHER INFORMATION: Synthetically generated proteins
 ;US-10-176-664-9

Query Match Best Local Similarity 84.5%; Score 1569.5; DB 14; Length 341; Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1; Db 1 EFPHHHHHTLSPESQVTIIPPTVKLFHSSCDPRGDAHSTIQOLICLVSQSPAKHVTW 60

Query 1 EFPHHHHHTLSPESQVTIIPPTVKLFHSSCDPRGDAHSTIQOLICLVSQSPAKHVTW 60
 QY 61 LVDGQEAENLPPYTRPKREGQTSLSQSEVNITQGOMMSNTYCHVKINGSIFEDSSR 120
 Db 1 LVDGQEAENLPPYTRPKREGQTSLSQSEVNITQGOMMSNTYCHVKINGSIFEDSSR 120

Query 121 KCADSNRGVSAYLSRSPPFDLPIRKSPPTICLVDLAPSKGTIVLUTWSRASGKVNHT 180
 Db 121 RSDDRERGVYTLIPSPDLYENGTPKUCLVLDL-ESEBNTITWWRBKSIGAS 179

Query 181 RKEEKONGTLTSTLPGVGDWLRGETQCRVTHPRALMSTKPGKLAPEVY 240
 Db 180 QRSKHHHTTSITSLPVDAKDWIGEGYQCRVDPHPRKPIVRSITKPGKLAPEVY 239

Query 241 MLPPSPBETGTRTVCILRGPYPSISVQMLPNBEDHGTHTTRPQDHGTPSPFL 300
 Db 240 MLPPSPBETGTRTVCILRGPYPSISVQMLPNBEDHGTHTTRPQDHGTPSPFL 299

Query 301 YSRMLVVKSIWKGNLVTCRVHEALPGSRTEKLSLYHAGN 342
 Db 300 YSRMLVVKSIWKGNLVTCRVHEALPGSRTEKLSLYHAGN 341

RESULT 12 US-10-176-664-4
 ; Sequence 4, Application US/10176664
 ; Publication No. US20030031663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Heilman, Lars T.
 ; TITLE OF INVENTION: ENHANCED VACCINES
 ; FILE REFERENCE: 10223/006001
 ; CURRENT APPLICATION NUMBER: US/10/176,664
 ; PRIOR FILING DATE: 2002-06-19
 ; PRIOR APPLICATION NUMBER: US/09/401,636
 ; PRIORITY NUMBER: US 60/106,652
 ; PRIORITY FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 341
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE: OTHER INFORMATION: Synthetically generated proteins
 ;US-10-176-664-4

Query Match Best Local Similarity 83.7%; Score 1553.5; DB 14; Length 341; Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1; Db 1 EFPHHHHHTLSPESQVTIIPPTVKLFHSSCDPRGDAHSTIQOLICLVSQSPAKHVTW 60

Query 1 EFPHHHHHTLSPESQVTIIPPTVKLFHSSCDPRGDAHSTIQOLICLVSQSPAKHVTW 60
 QY 61 LVDGQEAENLPPYTRPKREGQTSLSQSEVNITQGOMMSNTYCHVKINGSIFEDSSR 120
 Db 61 LVDGQEAENLPPYTRPKREGQTSLSQSEVNITQGOMMSNTYCHVKINGSIFEDSSR 120

Query 121 KCADSNRGVSAYLSRSPPFDLPIRKSPPTICLVDLAPSKGTIVLUTWSRASGKVNHT 180
 Db 121 RSDDRERGVYTLIPSPDLYENGTPKUCLVLDL-ESEBNTITWWRBKSIGAS 179

Query 181 RKEEKONGTLTSTLPGVGDWLRGETQCRVTHPRALMSTKPGKLAPEVY 240
 Db 180 QRSKHHHTTSITSLPVDAKDWIGEGYQCRVDPHPRKPIVRSITKPGKLAPEVY 239

Query 241 MLPPSPBETGTRTVCILRGPYPSISVQMLPNBEDHGTHTTRPQDHGTPSPFL 300
 Db 240 MLPPSPBETGTRTVCILRGPYPSISVQMLPNBEDHGTHTTRPQDHGTPSPFL 299

Query 301 YSRMLVVKSIWKGNLVTCRVHEALPGSRTEKLSLYHAGN 342
 Db 300 YSRMLVVKSIWKGNLVTCRVHEALPGSRTEKLSLYHAGN 341

RESULT 13
; Sequence 6, Application US/09401636
; Patent No. US2001018843A1
; GENERAL INFORMATION:
; APPLICANT: Hallman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: US/01/636-6
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-6

Query Match 82.4%; Score 1528.5; DB 9; Length 341;
Best Local Similarity 83.0%; Pred. No. 2.9e-11.9; Mismatches 43; Indels 1; Gaps 1;
Matches 284; Conservative 14; MisMatched 43; Indels 1; Gaps 1;
Query 1 EFHHHHHHTLISLPSBSPGVTIIPPTVKLFHSSCDPREGAHTSTIQOLCLVLSGFSPAKVTW 60
Db 1 EFHHHHHHTLISLPSBSPGVTIIPPTVKLFHSSCDPREGAHTSTIQOLCLVLSGFSPAKVTW 60
Query 61 LVDGQEAENLFPYTRPKREGGOTFSILOSEVNITOGOMMSNTYTCVKHNGSIEFESSR 120
Db 61 LVDGQEAENLFPYTRPKREGGOTFSILOSEVNITOGOMMSNTYTCVKHNGSIEFESSR 120
Query 121 KCAASNPRGVSAYLSPSPDFLIRKPTITCILVPLSKGKVNLTWSRASGKPNHST 180
Db 121 KCAASNPRGVSAYLSPSPDFLIRKPTITCILVPLSKGKVNLTWSRASGKPNHST 180
Query 121 RCPDHPERPVITLIPSPDLIYONGAKPLTCLVUDLESEK-NVNNTWNQEKTSVNASQ 179
Db 121 RCPDHPERPVITLIPSPDLIYONGAKPLTCLVUDLESEK-NVNNTWNQEKTSVNASQ 179
Query 181 RKEBKQRGQTLYTISTVLTGTRWIEGTYTQCRVTHPLPRALMRSTIKLUGKRLAPEVY 240
Db 181 RKEBKQRGQTLYTISTVLTGTRWIEGTYTQCRVTHPLPRALMRSTIKLUGKRLAPEVY 240
Query 180 WYTKHNNATTSISLISLFWAKWIEGYQOCVTDHPDPKPKIVRSITKLPKRLAPEVY 239
Db 180 WYTKHNNATTSISLISLFWAKWIEGYQOCVTDHPDPKPKIVRSITKLPKRLAPEVY 239
Query 241 MLPPSPPEEGTTRTVCIRGFYSESVQWLENNEHDHTHTTRPKQHGTSPFL 300
Db 240 MLPPSPPEEGTTRTVCIRGFYSESVQWLPNNEHDHTHTTRPKQHGTSPFL 299
Query 301 YSRMLVNLNSIWEKONLIVCRVHAEALPSRTLEKSLHYSAGN 342
Db 300 YSRMLVNLNSIWEKONLIVCRVHAEALPSRTLEKSLHYSAGN 341
RESULT 14
; Sequence 6, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-401-636-6

Query Match 82.4%; Score 1528.5; DB 9; Length 341;
Best Local Similarity 83.0%; Pred. No. 2.9e-11.9; Mismatches 43; Indels 1; Gaps 1;
Matches 284; Conservative 14; MisMatched 43; Indels 1; Gaps 1;
Query 1 EFHHHHHHTLISLPSBSPGVTIIPPTVKLFHSSCDPREGAHTSTIQOLCLVLSGFSPAKVTW 60
Db 1 EFHHHHHHTLISLPSBSPGVTIIPPTVKLFHSSCDPREGAHTSTIQOLCLVLSGFSPAKVTW 60
Query 61 LVDGQEAENLFPYTRPKREGGOTFSILOSEVNITOGOMMSNTYTCVKHNGSIEFESSR 120
Db 61 LVDGQEAENLFPYTRPKREGGOTFSILOSEVNITOGOMMSNTYTCVKHNGSIEFESSR 120
Query 121 KCAASNPRGVSAYLSPSPDFLIRKPTITCILVPLSKGKVNLTWSRASGKPNHST 180
Db 121 KCAASNPRGVSAYLSPSPDFLIRKPTITCILVPLSKGKVNLTWSRASGKPNHST 180
Query 121 RCPDHPERPVITLIPSPDLIYONGAKPLTCLVUDLESEK-NVNNTWNQEKTSVNASQ 179
Db 121 RCPDHPERPVITLIPSPDLIYONGAKPLTCLVUDLESEK-NVNNTWNQEKTSVNASQ 179
Query 181 RKEBKQRGQTLYTISTVLTGTRWIEGTYTQCRVTHPLPRALMRSTIKLUGKRLAPEVY 240
Db 181 RKEBKQRGQTLYTISTVLTGTRWIEGTYTQCRVTHPLPRALMRSTIKLUGKRLAPEVY 240
Query 180 WYTKHNNATTSISLISLFWAKWIEGYQOCVTDHPDPKPKIVRSITKLPKRLAPEVY 239
Db 180 WYTKHNNATTSISLISLFWAKWIEGYQOCVTDHPDPKPKIVRSITKLPKRLAPEVY 239
Query 241 MLPPSPPEEGTTRTVCIRGFYSESVQWLENNEHDHTHTTRPKQHGTSPFL 300
Db 240 MLPPSPPEEGTTRTVCIRGFYSESVQWLPNNEHDHTHTTRPKQHGTSPFL 299
Query 301 YSRMLVNLNSIWEKONLIVCRVHAEALPSRTLEKSLHYSAGN 342
Db 300 YSRMLVNLNSIWEKONLIVCRVHAEALPSRTLEKSLHYSAGN 341
RESULT 15
; Sequence 32, Application US/0214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGM-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Opossum (*Monodelphis domestica*)
; US-10-214-524-32

Query Match 82.1%; Score 1523.5; DB 14; Length 446;
Best Local Similarity 84.7%; Pred. No. 1.1e-11.8; Mismatches 23; Indels 1; Gaps 1;
Matches 283; Conservative 21; MisMatches 23; Indels 1; Gaps 1;
Query 9 TLSLPSPESGTTRTVCIRGFYSESVQWLENNEHDHTHTTRPKQHGTSPFL 68
Db 114 TLSLPSPECGVITLIPPTVKLFHSSCDPREGAHTSTIQOLCLVLSGFSPAKVTWLVDCGAE 173
Query 69 NLFLYTTTRPKREGGOTFSILOSEVNITOGOMMSNTYTCVKHNGSFPEDSRKCAISNPR 128
Db 174 NLFLYTTTRPKREGGOTFSILOSEVNITOGOMMSNTYTCVKHNGSFPEDSRKCAISNPR 123
Query 129 GVSAYLRSRSPSPDFLIRKPTITCILVPLSKGKVNLTWSRASGKVNHSRKEKORN 188
Db 234 GISAVILPPTPDLIYONGAKPLTCLVUDLESAENVYKWTWSRESGGPVNPSLIVKQYN 292
Query 189 GILTWTSTIPGDRWIEGTYTQCRVTHPLPRALMRSTIKLUGKRLAPEVYMLPPSPEE 248

Db 293 GPPTVNHLPPVNTDDWIEGDYTCRLESPPDMVPLRTISKAPGRKLAPEVYMLPPSPB 352
QY 249 TGTTRTVTCLLRGFYSEISYOWLFFNNEDITGHMTTRQKDHDNDPSFLYRMLVAK 308
Db 353 TGTTRTVTCLLRGFYSEISYOWLFFNNEDITGHMTTRQKDHDNDPSFLYRMLVAK 412
QY 309 SIWEKGMLVTCRWHALPGERTLEKSLHAGN 342
Db 413 SIWEKGMLVTCRWHALPGSTLEKSLHAGN 446

Search completed: February 26, 2004, 12:05:55
Job time : 39 secs

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GenCore version 5.1.5

IM protein - protein search, using sw model

run on: February 26, 2004, 11:42:41 ; Search time 59 Seconds

perfect score: 1855

sequence: 1 EFFFFHHHTLSPBESGPVTL.....HEALPGSRTLEKLSLHYSAGN 342

scoring table: BLOSUM62

GapOp 10.0 , GapExt 0.5

searched: 1586107 seqs, 282547505 residues

total number of hits satisfying chosen parameters: 1586107

minimum DB seq length: 0

maximum DB seq length: 200000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : A_Geneseq_29Jan04:*

1: geneseqP19008:*

2: geneseqP19008:*

3: geneseqP20008:*

4: geneseqP20018:*

5: geneseqP20028:*

6: geneseqP003ab:*

7: geneseqP2003bs:*

8: geneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1856	100.0	342	3 AAB06205	Ab06205 Immunogen
2	1644.5	88.6	341	3 AAB06208	Ab06208 Immunogen
3	1587.5	85.5	345	3 AAB06207	Ab06207 Immunogen
4	1584.5	85.4	341	3 AAB03544	Ab03544 Opossum
5	1568.5	84.5	341	3 AAB06206	Ab06206 Immunogen
6	1523.5	82.1	446	6 ABB96587	Abp96587 Opossum
7	1392.5	75.0	341	3 AAB06202	Ab06202 Immunogen
8	1375	74.1	342	3 AAB06201	Ab06201 Immunogen
9	1289.5	69.3	427	6 ABB96591	Abp96591 Brushtail
10	1045.5	56.9	569	6 AAO19668	AAO19668 G32 fushi
11	1044	56.2	577	6 ABB96594	Abp96594 Duckbill
12	1038.5	56.0	320	6 AAO19667	AAO19667 Human IgG
13	1038.5	56.0	323	5 AAB08286	Aab08286 Human IgG
14	1038.5	56.0	323	5 AAB08285	Aab08285 Human IgG
15	1038.5	56.0	323	5 AAB08284	Aab08284 Human IgG
16	1038.5	56.0	324	5 AAB08283	Aab08283 Human IgG
17	1038.5	56.0	325	2 AAB75225	Ab75225 Human IgG
18	1038.5	56.0	325	2 AAB77241	Ab77241 Human IgG
19	1038.5	56.0	331	3 AAB03642	Ab03642 Human IgG
20	1038.5	56.0	331	7 ABB25768	Abp25768 Binding
21	1038.5	56.0	367	2 AAB08021	Aab08021 Interleukin
22	1038.5	56.0	427	6 AAO19665	AAO19665 Human IgG
23	1038.5	56.0	428	5 AAM47863	Aam47863 Human IgG
24	1038.5	56.0	428	5 AAB02833	Aab02833 Human IgG
25	1038.5	56.0	428	5 AAM05940	Aam05940 Human IgG

26	1038.5	55.6	428	6	ABP35113	Human IgM
27	1038.5	55.6	428	7	ADD48440	Human Pro
28	1038.5	55.6	574	5	ABG94550	Abg94550 Human IgE
29	1038.5	55.6	574	5	ABG80562	Abg80562 Human IgE
30	1038.5	55.6	574	6	ABP96592	Abp96592 Human IgE
31	1038.5	55.6	592	7	ADD25773	Add25773 Binding d
32	1036.5	55.8	330	5	ABU80289	Abu80289 Human IgE
33	1035.5	55.8	325	3	RAY79994	Ray79994 Human IgM
34	1034.5	55.8	336	5	AAUB0287	AAUB0287 Human IgE
35	1034.5	55.7	441	5	AAUP40065	AAUP40065 Sequence
36	1030.5	55.5	493	1	ABP96581	ABP96581 Chimpanze
37	1024.5	55.2	426	6	ABR85582	ABR85582 IgC (eps110
38	1019.5	54.9	315	2	ABR83582	ABR83582 CH2 to CH
39	1019.5	54.9	325	2	AAE35114	AAE35114 Human IgM
40	1010.5	54.4	425	6	Aar42950	Aar42950 Human IgE
41	1002.5	54.0	428	2	ABR42950	ABR42950 Human IgE
42	996.5	53.7	347	6	ABG74784	ABG74784 Human IgE
43	992.5	53.5	343	3	ABP06204	ABP06204 Platypus
44	989	53.3	426	6	ABP96583	ABP96583 Dog IgE h
45	978	52.7	496	6	ABP96580	ABP96580 Cat IgE h
ALIGNMENTS						
RESULT 1						
ABP0605	ABP06205	standard; protein; 342 AA.				
XX	XX					
AC	AC					
XX	XX					
DT	DT	12-SEP-2003 (revised)				
DT	DT	22-NOV-2000 (first entry)				
DE	DE	Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.				
XX	XX	Human; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;				
KW	KW	asthma; eczema; immunogenic peptide.				
XX	XX	Didelphis virginiana.				
OS	OS	Homo sapiens.				
OS	OS	Chimeric.				
XX	XX	WO200025722-A2.				
XX	XX	11-MAY-2000.				
PP	PP	99WO-SE001896.				
XX	XX	21-OCT-1999;				
PR	PR	02-NOV-1998; 98US-0106652P.				
XX	XX	22-SEP-1999; 99US-00401636.				
PA	PA	(RESI-) RESISTENTIA PHARM AB.				
XX	PT	Pi Hellman LT;				
XX	DR	WPI; 2000-365342/31.				
XX	PT	Immunogenic polypeptides useful for preventing the harmful effects of				
XX	PT	immunoglobulin E in mammals.				
PS	PS	Disclosure; Fig 2; 50pp; English.				
XX	XX	The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the human. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.				
CC	CC	(Updated on 12-SEP-2003 to standardise OS field)				

PA	(REST-)	RESISTENTIA PHARM AB.	XX
XX			XX
PI	Hellman LT;		XX
XX			XX
DR	WPI; 2000-365342/31.		PR
XX			PF
PT	Immunogenic polypeptides useful for preventing the harmful effects of		XX
PT	immunoglobulin E in mammals.		XX
XX			PA
PS	Disclosure; Fig 2; 50pp; English.		XX
XX			PI
CC	The present sequence is an immunogenic peptide consisting of the heavy		XX
CC	chain constant regions 2 and 4 of the opossum IgE and the heavy chain		DR
CC	constant region 3 from the rat. It was shown to cause a stronger		XX
CC	polyclonal anti-self IgE response than peptides consisting of the same		PR
CC	regions from one mammal. Immunogenic peptides, particularly those		XX
CC	consisting of different heavy chain constant regions, can be used for		PA
CC	vaccination in humans, against bacterial and viral infections and		XX
CC	allergies, such as asthma, fur, pollen and food allergies and eczema.		PT
CC	(Updated on 12-SEP-2003 to standardise OS field)		XX
XX			PS
SQ	Sequence 341 AA;		XX
Query Match	84.5%; Score 1568.5; DB 3; Length 341;		CC
Best Local Similarity	83.3%; Pred. No. 3.3e-122;		CC
Matches	285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;		CC
QY	1 EFRHHHHHTLSPESGPVITIPIPTVKLFHSSCDPRAHSNTQOLGLVSGSPAKHVTW 60		CC
Db	1 EFRHHHHHTLSPESGPVITIPIPTVKLFHSSCDPRAHSNTQOLGLVSGSPAKHVTW 60		CC
QY	61 LVDQGAENLFPPTPRREGGOTFSIQSEVNITQGOMMSNTYCHVKHNGSFEDSSR 120		CC
Db	61 LVDQGAENLFPPTPRREGGOTFSIQSEVNITQGOMMSNTYCHVKHNGSFEDSSR 120		CC
QY	121 KCDANPQGSAVLSRSPDPIFIRKSPITPLVDAPIPSKQVTVNWSRAGKVNHST 180		CC
Db	121 KCDANPQGSAVLSRSPDPIFIRKSPITPLVDAPIPSKQVTVNWSRAGKVNHST 180		CC
QY	121 RSDDEPGRVITLIPSPDLYENGSPKPLVLDI-ESSENITTVWKRKSGAS 179		CC
Db	121 RSDDEPGRVITLIPSPDLYENGSPKPLVLDI-ESSENITTVWKRKSGAS 179		CC
QY	181 RKEKERRQNTLAVTSTPVGTRADMEATYQCRVTHPHPRALMRSTKLPGKLAPEVY 240		CC
Db	180 QRTKHNATTSITSLRVDADWIESEYQCRVDRHPRREVTSITKPGKLAPEVY 239		CC
QY	241 MPPSPPEBTGTTVTCUCLRGYPSISVQMLFNNEEDHTGHTTRPQDHGTDPSFEL 300		CC
Db	240 MPPSPPEBTGTTVTCUCLRGYPSISVQMLFNNEEDHTGHTTRPQDHGTDPSFEL 299		CC
QY	301 YSPMLVUNISIWEKGNLVTCRVHEALGSRTEKSLHYSAGN 342		CC
Db	300 YSPMLVUNISIWEKGNLVTCRVHEALGSRTEKSLHYSAGN 341		CC
SQ	Sequence 446 AA;		XX
Query Match	82.1%; Score 1523.5; DB 6; Length 446;		XX
Best Local Similarity	81.7%; Pred. No. 2.6e-118;		XX
Matches	283; Conservative 21; Mismatches 29; Indels 1; Gaps 1;		XX
QY	9 TSLPESGPVITIPIPTVKLFHSSCDPRAHSNTQOLGLVSGSPAKHVTWLGCEAE 68		XX
Db	9 TSLPESGPVITIPIPTVKLFHSSCDPRAHSNTQOLGLVSGSPAKHVTWLGCEAE 68		XX
QY	114 TSLPESGPVITIPIPTVKLFHSSCDPRAHSNTQOLGLVSGSPAKHVTWLGCEAE 173		XX
Db	114 TSLPESGPVITIPIPTVKLFHSSCDPRAHSNTQOLGLVSGSPAKHVTWLGCEAE 173		XX
QY	69 NLFPYTRPRREGGOTFSIQSEVNITQGOMMSNTYCHVKHNGSFEDSSRKAQDSNPR 128		XX
Db	174 NLFPYTRPRREGGOTFSIQSEVNITQGOMMSNTYCHVKHNGSFEDSSRKAQDSNPR 123		XX
QY	129 GVASILSRSPDPIFIRKSPITPLVDAPIPSKQVTVNWSRAGKVNHSTKEKQRN 188		XX
Db	129 GVASILSRSPDPIFIRKSPITPLVDAPIPSKQVTVNWSRAGKVNHSTKEKQRN 188		XX
QY	234 GIAVILPPTPQDVKVQPTGCLVDA-SAENVYTVWRSCEGPVNPSSVWQEQN 292		XX
Db	189 GTLVTSTPVGTRDMEATYQCRVTHPHPRALMRSTKLPGKLAPEVYMLPSPEE 248		XX
Db	293 GTLVTSTPVGTRDMEATYQCRVTHPHPRALMRSTKLPGKLAPEVYMLPSPEE 352		XX
QY	249 TGTRTVCLRGYPSISVQMLFNNEEDHTGHTTRPQDHGTDPSFLYSLRMLVNK 308		XX
Db	353 TGTRTVCLRGYPSISVQMLFNNEEDHTGHTTRPQDHGTDPSFLYSLRMLVNK 412		XX
QY	309 SIEKGNLWTCRVHEALGSRTEKSLHYSAGN 342		XX

Db	RESULT 7	RK-EKQRONGITLTVTISTLPVGRDMEGETYQCRVTHPLPRALEMSTTKUFGKRLAPE	238
ID	AAB06202	;	;
XX	AAB06202 standard; protein; 341 AA.	;	;
AC	AAB06202;	;	;
XX		;	;
DT	12-SEP-2003 (revised)	;	;
DT	22-NOV-2000 (first entry)	;	;
XX	Immunogenic peptide consisting of opossum CH ₂ , mouse CH ₃ and opossum CH ₄ .	;	;
XX	Mouse; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;	;	;
KW	asthma; eczema; immunogenic peptide.	;	;
XX	Didelphis virginiana.	;	;
OS	Mus sp.	;	;
OS	Chimeric.	;	;
XX		;	;
FH		;	;
FT	Key	Location/Qualifiers	
FT	Misc-difference 1. 341	/label= OTHER	
FT	/note= "Xaa=unknown"		
FT	;	;	;
XX	WMLPPSBEITGATRTVTCILRGCFYPSITSVQMLFNNEBEDHTGHHTTRPQXDHGTFPSF	239	
XX	VMLPPSBEITGATRTVTCILRGCFYPSITSVQMLFNNEBEDHTGHHTTRPQXDHGTFPSF	238	
PN	WO200025722-A2.	;	;
PD	11-MAY-2000.	;	;
PA	21-OCT-1999;	99WO-SE001896.	
PP	02-NOV-1998;	98US-010652P.	
PR	22-SEP-1999;	99US-00401636.	
XX		;	;
XX	(RESI-) RESISTENTIA PHARM AB.	;	;
XX	PT	;	;
PT	PT	;	;
XX	Immunogenic polypeptides useful for preventing the harmful effects of	;	;
XX	immunoglobulin E in mammals.	;	;
PS	Disclosure; Fig 2; 50pp; English.	;	;
XX		;	;
XX	The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 3 from the mouse. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)	;	;
CC	Sequence 341 AA;	;	;
SQ	Query Match 75.0%; Score 1392.5; DB 3; Length 341; Best Local Similarity 76.7%; Pred. No. 1.5e-107; Matches 263; Conservative 22; Mismatches 53; Indels 5; Gaps 3;	;	;
CC	Chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 created from a combination of the one from the rat and the one from the opossum. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)	;	;
XX	Sequence 342 AA;	;	;
PS	Disclosure; Fig 2; 50pp; English.	;	;
XX		;	;
CC	The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 created from a combination of the one from the rat and the one from the opossum. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)	;	;
XX	Sequence 342 AA;	;	;
PS	Disclosure; Fig 2; 50pp; English.	;	;
XX		;	;
CC	The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 created from a combination of the one from the rat and the one from the opossum. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)	;	;
XX	Sequence 342 AA;	;	;
CC	Query Match 74.1%; Score 1375; DB 3; Length 342; Best Local Similarity 76.6%; Pred. No. 4.4e-106; Matches 22; Conservative 22; Mismatches 55; Indels 2; Gaps 2;	;	;
DB	121 KCDASDPRGVASYLSRSPSPFPLFIRKSPITCLVWDLAFPSKGTLNTLWSRASGKPVNHF	180	
DB	121 RCPDPHPRGVYTLIPPSPLDYLQIGAKPLTCVLDLREK-HINTVWOR--KPTXXXA	177	
DB	61 LVDGQAEALNLYPTTPKREGQTSVLSQEVNITQWMSNTVTCIHWGNSFEDSR	120	
DB	61 LVDGQAEALNLYPTTPKREGQTSVLSQEVNITQWMSNTVTCIHWGNSFEDSR	120	
DB	121 KCDASDPRGVASYLSRSPSPFPLFIRKSPITCLVWDLAFPSKGTLNTLWSRASGKPVNHF	180	
DB	121 RCPDPHPRGVYTLIPPSPLDYLQIGAKPLTCVLDLREK-HINTVWOR--KPTXXXA	177	

QY 1 EPRHHHRHTLSIPESGPVTLIIPPTVKGFLHSCDPGDAHSTIQOLICLYSGFSPAKVATW 60
 CC 1 EPRHHHRHTLSIPESGPVTLIIPPTVKGFLHSCDPGDAHSTIQOLICLYSGFSPAKVATW 60
 Db 61 LVDGQEAENLFPTTAKREGQTSIQLSEVNTIGOMMSNTVTCYKNGSIFPSSR 120
 QY 61 LVDGQEAENLFPTTAKREGQTSIQLSEVNTIGOMMSNTVTCYKNGSIFPSSR 120
 Db 121 KCADSNFRGVSAVLRSRSPFDLFLRKSPPTCLVVDLAKSKGTVNLWSRACKPVHST 180
 QY 121 KCADSNFRGVSAVLRSRSPFDLFLRKSPPTCLVVDLAKSKGTVNLWSRACKPVHST 180
 Db 121 RSDDEPRGVITYLIPSPDLYERGTPKTCVLDL EBBHIXVTVXERPKXIKAR 179
 QY 181 RKEKQ-NGTITVTSPLPVOTRDWIEGETYOCRVTHPHPRALMRSTKLGKRLAPEV 239
 Db 180 SUVVKENHGFTXTSHLPIZDDNIEGXVYTXLESPDWIVLILPTISALPEKRLAPXV 239
 QY 240 YMLPPSPEETXTTRTICLARGFYFSEISYQWLFKXEDHTIGHITTRPQDQHGDIXSFP 299
 Db 240 YMLPPSPEETXTTRTICLARGFYFSEISYQWLFKXEDHTIGHITTRPQDQHGDIXSFP 299

LYSRMLNKS1WEKGNLVTRVHAPLSPRTLSKLYSAG 341

Db 300 LYSRMLNKS1WEKGNLVTRVHAPLSPRTLSKLYSAG 341

RESULT 9

QY 1 EPRHHHRHTLSIPESGPVTLIIPPTVKGFLHSCDPGDAHSTIQOLICLYSGFSPAKVATW 60
 CC 1 EPRHHHRHTLSIPESGPVTLIIPPTVKGFLHSCDPGDAHSTIQOLICLYSGFSPAKVATW 60
 CC (C2) comprising at least one isolated polynucleotide encoding (1), and
 CC (C3) comprising antigen-presenting cells that recognise at least one (1).
 CC Where (C3) are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IGE peptides, (C1-3) have antiallergic, antiasthmatic, immunosuppressive,
 CC vasoconstrictive, dermatological, antiinflammatory and cytotoxic activities,
 CC and can be used as inducers of a CTL response against IGE, and in
 CC vaccines. (C1-3) can be used for modulating an IGE-mediated condition in a
 CC mammal. (C1-3) are useful for modulating an IGE-mediated condition such as
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, (C1-3) are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IGE heavy chain amino acid
 CC sequence, which is given in an example from the present invention

SQ

XX

CC heavy chain constant region CH2-CH3-CH4 portion
 XX
 SQ Sequence 320 AA;
 Query Match 56.0%; Score 1038.5; DB 6; Length 320;
 Best Local Similarity 62.4%; Pred. No. 4-3a-78;
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;
 XX
 QY 199 VGRDRMVEGETYQCRVTHPLPRLMRSTKPGKRAPEVMLPPSPEET--GTRT 256
 DB 433 UNIQDNEGEGSYTCRVAHDLSPIKTVKPGKRAPEVAPPPQAEVSHGSSLT 492
 QY 257 CLIRGPYPSISVOMLNRRNEDHTGHHTTRPQDKHDGNDPSEFLYRSLVNLVNSIMBGNL 316
 DB 493 CLIRGPYPSISVOMLNRRNEDHTGHHTTRPQDKHDGNDPSEFLYRSLVNLVNSIMBGNL 552
 QY 317 VTCRVRVHEALPGSRTEKLSLHYSAGN 342
 DB 553 YTCQVVHEALP-SRVERKFOHTSGN 577
 QY RESULT 12
 AAO19667
 ID AAO19667 standard; protein; 320 AA.
 AC AAO19667;
 XX
 DT 28-MAR-2003 (first entry)
 XX Human IgE heavy chain constant region CH2-CH3-CH4 portion.
 XX Human: IgE; immunoglobulin E; immunotherapy; immune disease;
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
 KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;
 KW CH2-CH3-CH4 region.
 XX
 OS Homo sapiens.
 PN WO200288317-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 01-MAY-2002; 2002WO-US013527.
 PR 01-MAY-2001; 2001US-00847208.
 PR 24-OCT-2001; 2001US-0000439.
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Saxon A, Zhang K, Zhu D;
 XX
 DR WPI; 2003-103456/09.
 XX
 PT New fusion molecules comprising polypeptide sequences that bind to IgE
 PT inhibitory receptor and native IgE receptor, useful for treating IgE-
 mediated hypersensitivity reactions, e.g. asthma or allergies, or
 PT autoimmune diseases.
 PT
 PS Claim 21; Fig 6; 116PP; English.
 XX
 CC The present invention relates to a fusion molecule comprising a first
 CC polypeptide sequence capable of specific binding to a native IgE
 CC inhibitory receptor consisting of an immune receptor tyrosine-based
 CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
 CC functionally connected to a second polypeptide sequence capable of
 CC specific binding directly or indirectly to a native IgE receptor
 (Fc epsilon R). Also provided are nucleotide sequences encoding such a
 CC fusion protein. The fusion molecules and compositions are useful for
 CC treating an IgE-mediated biological response, preferably an IgE-mediated
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
 CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,
 CC or symptoms resulting from, a type I hypersensitivity reaction in a
 CC subject receiving immunotherapy. The present sequence is the human IgE
 CC
 XX
 QY 139 PFDLIRKSPITCLVWDLAPSKGTIVNLITWSRASKGKVNHSRKEEKQRNGTILTIVTSLP 198
 DB 374 PTDLVSKTKEKLTCIILIDVSTG-MEVVWSRSRGTLSASSEEDQKQFNGTMSFISTPV 432
 QY 199 VGRDRMVEGETYQCRVTHPLPRLMRSTKPGKRAPEVMLPPSPEET--GTRT 256
 DB 433 UNIQDNEGEGSYTCRVAHDLSPIKTVKPGKRAPEVAPPPQAEVSHGSSLT 492
 QY 257 CLIRGPYPSISVOMLNRRNEDHTGHHTTRPQDKHDGNDPSEFLYRSLVNLVNSIMBGNL 316
 DB 493 CLIRGPYPSISVOMLNRRNEDHTGHHTTRPQDKHDGNDPSEFLYRSLVNLVNSIMBGNL 552
 QY 317 VTCRVRVHEALPGSRTEKLSLHYSAGN 342
 DB 553 YTCQVVHEALP-SRVERKFOHTSGN 577
 QY RESULT 12
 AAO19667
 ID AAO19667 standard; protein; 320 AA.
 AC AAO19667;
 XX
 DT 28-MAR-2003 (first entry)
 XX Human IgE heavy chain constant region CH2-CH3-CH4 portion.
 XX Human: IgE; immunoglobulin E; immunotherapy; immune disease;
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
 KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;
 KW CH2-CH3-CH4 region.
 XX
 OS Homo sapiens.
 PN WO200288317-A2.
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 PD 07-NOV-2002.
 XX
 PF 01-MAY-2002; 2002WO-US013527.
 PR 01-MAY-2001; 2001US-00847208.
 PR 24-OCT-2001; 2001US-0000439.
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 CC dermatitis, severe food allergies, chronic urticaria, angioedema or
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
 CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,
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 CC subject receiving immunotherapy. The present sequence is the human IgE
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 DB 433 UNIQDNEGEGSYTCRVAHDLSPIKTVKPGKRAPEVAPPPQAEVSHGSSLT 492
 QY 257 CLIRGPYPSISVOMLNRRNEDHTGHHTTRPQDKHDGNDPSEFLYRSLVNLVNSIMBGNL 316
 DB 493 CLIRGPYPSISVOMLNRRNEDHTGHHTTRPQDKHDGNDPSEFLYRSLVNLVNSIMBGNL 552
 QY 317 VTCRVRVHEALPGSRTEKLSLHYSAGN 342
 DB 553 YTCQVVHEALP-SRVERKFOHTSGN 577
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 ID AAO19667 standard; protein; 320 AA.
 AC AAO19667;
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 DT 28-MAR-2003 (first entry)
 XX Human IgE heavy chain constant region CH2-CH3-CH4 portion.
 XX Human: IgE; immunoglobulin E; immunotherapy; immune disease;
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
 KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
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 PN WO200288317-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 01-MAY-2002; 2002WO-US013527.
 PR 01-MAY-2001; 2001US-00847208.
 PR 24-OCT-2001; 2001US-0000439.
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 PI Saxon A, Zhang K, Zhu D;
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 DR WPI; 2003-103456/09.
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 CC dermatitis, severe food allergies, chronic urticaria, angioedema or
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 DB 374 PTDLVSKTKEKLTCIILIDVSTG-MEVVWSRSRGTLSASSEEDQKQFNGTMSFISTPV 432
 QY 199 VGRDRMVEGETYQCRVTHPLPRLMRSTKPGKRAPEVMLPPSPEET--GTRT 256
 DB 433 UNIQDNEGEGSYTCRVAHDLSPIKTVKPGKRAPEVAPPPQAEVSHGSSLT 492
 QY 257 CLIRGPYPSISVOMLNRRNEDHTGHHTTRPQDKHDGNDPSEFLYRSLVNLVNSIMBGNL 316
 DB 493 CLIRGPYPSISVOMLNRRNEDHTGHHTTRPQDKHDGNDPSEFLYRSLVNLVNSIMBGNL 552
 QY 317 VTCRVRVHEALPGSRTEKLSLHYSAGN 342
 DB 553 YTCQVVHEALP-SRVERKFOHTSGN 577
 QY RESULT 13
 AAB80286
 ID AAB80286 standard; protein; 323 AA.
 AC AAB80286;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DB Human IgE C2-C3-C4 domain for E.Coli expression.
 XX
 KW IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
 KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200220038-A2.
 XX
 PD 14-MAR-2002.
 PR 06-SEP-2001; 2001WO-DK000579.
 PR 06-SEP-2000; 2000DK-0001326.
 PR 15-SEP-2000; 2000US-0232831P.
 XX
 PA (Pfizer) PHARMEXA AS.
 XX
 PI Klynsner S, von Hoegen P, Voldborg B, Gautam A;
 XX
 DR WPI; 2002-383034/41.
 DR N-PSDB; ABK51134.
 XX
 PT Inducing immune response against autologous immunoglobulin E in an
 PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
 PT epitope an/or B-cell epitope derived from the immunoglobulin.
 XX
 PS Disclosure; Page 112-113; 151PP; English.
 XX

This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (Th epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains optimised for expression in an *E. coli* system, this sequence was used to create the epitopes of the invention.

(PHAR-) PHARMEXA AS.
Klybner S, Von Hoegen P, Voldborg B, Gautam A;
WPI: 2002-383033/11.
N-PSDB; ARKS1133.

Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.

disclosure; page 100-101; 134pp; August.

This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte

SQ Sequence 323 AA;

Db	124	LFRKSPPTTCLUVVLDLASSKGTVNNTWRSAGKVNHSRKECORNGLTIVTSTLPGT	QY	183
Db	202	RDMIEGETYQCRVTHPHLPRALMSTKLUKGKLAPEVNLPPPEEETGT--TRTVCLJ	QY	259
Db	184	RDWIEGETYQCRVTHPHLPRALMSTKLUKGKLAPEVNLPPPEEETGT--TRTVCLJ	QY	242
QY	260	RGYPPSEISQWILENEEDHTGHTTTRQDKHETDPSFLYRLVNLVNSIWEKGNLVTC	QY	319
Db	243	QNTMPEDISQWILHNEQVLDPARHSTTQPRKGS--GPFVFSRLEVTRAEWQKDEFIC	QY	300
QY	320	RVVFELPGSRTLEKSKLHSAG	QY	341
Db	301	RATHEAASPQTVQRAVSTNG	Db	322

RESULT 14
ID AAU80285 standard; protein; 323 AA.
XX
AC AAU80285;
XX
DT 30-JUL-2002 (first entry)
DE Human IgE C2-C3-C4 domains for mammalian expression.
XX

XX	IGE; allergy; human; antiallergic; immuno suppressive; antianaphylactic;
KW	antiarrhythmic; dermatological; antiinflammatory; immunoglobulin E; IGE;
KW	antiautonomic; vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
KW	heavy chain C domain.
KX	
OS	Homo sapiens.
OS	Synthetic.
XX	
DN	

WO20020038-A2.

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 26, 2004, 11:57:11 ; Search time 45 Seconds

Sequence: 1. EFPHHHHHTLSPESGPVTL.....HEALPCSRTEKLSLHYSGAN 342

Scoring table: BLOSUM62

Gap0 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315318202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_25;*

1: sp_archea;*

2: sp_bacteria;*

3: sp_fungi;*

4: sp_human;*

5: sp_invertebrate;*

6: sp_mammal;*

7: sp_mhc;*

8: sp_organelle;*

9: sp_phage;*

10: sp_plant;*

11: sp_rabbit;*

12: sp_virus;*

13: sp_vertebrate;*

14: sp_unclassified;*

15: sp_rvirus;*

16: sp_bacteriap;*

17: sp_archeap;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	482.5	26.0	337 6 Q95M34	Q95m34 equus cabal
2	479.5	25.8	473 4 Q8TC63	Q8tc63 homo sapien
3	476	25.3	611 11 Q7TM05	Q7tm05 mus musculus
4	469	25.3	613 11 Q8VCX7	Q8vcx7 mus musculus
5	465	25.1	375 4 Q8ETTL	Q8ettl homo sapien
6	465	25.1	588 4 Q9BWU0	Q9bwu4 homo sapien
7	465	25.1	597 4 Q9BQB8	Q9bqb8 homo sapien
8	465	25.1	597 4 Q9BQB9	Q9bqb9 homo sapien
9	465	25.1	597 4 Q96BB9	Q96bb9 homo sapien
10	465	25.1	613 4 Q96EY0	Q96ey0 homo sapien
11	465	25.1	613 4 Q8WUK1	Q8wuk1 homo sapien
12	465	25.1	614 4 Q96GA6	Q96ga6 homo sapien
13	465	25.1	618 4 Q96AA6	Q96aa6 homo sapien
14	455	24.5	469 4 Q7Z7PS	Q7z7ps homo sapien
15	455	24.5	470 4 Q7Z5W1	Q7z5wi homo sapien
16	450	24.2	482 4 Q7Z351	Q7z351 homo sapien

17 446 24.0 521 4 Q8N4Y9 homo sapien

18 444 23.9 509 4 Q8NF17 homo sapien

19 441 23.8 354 4 Q8ETT2 homo sapien

20 440.5 23.7 437 11 Q9R1A4 musculus

21 440 23.7 463 11 Q99LC4 musculus

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23 421 22.7 473 11 Q9D8L4 musculus

24 402.5 21.7 679 4 Q96PQ8 homo sapien

25 399 21.5 468 11 Q99L31 musculus

26 399 21.5 473 11 Q99L25 musculus

27 398 21.4 470 11 Q7TMK1 musculus

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36 358 19.3 496 4 Q96KX8 homo sapien

37 358 19.3 497 4 Q8WY24 homo sapien

38 355.5 19.2 499 4 Q8N5K4 homo sapien

39 355 19.1 496 4 Q96D90 homo sapien

40 351.5 18.9 587 13 Q7T0R1 xenopus laevis

41 348 18.8 426 11 Q9DCD9 homo sapien

42 346 18.6 500 4 Q9BVO0 homo sapien

43 345 18.6 486 11 Q91Z07 homo sapien

44 345 18.6 487 11 Q99KA4 homo sapien

45 338.5 18.2 479 11 Q99M22 musculus

17 446 24.0 521 4 Q8N4Y9 homo sapien

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17 446 24.0 521 4 Q8N4Y9 homo sapien

18 444 23.9 509 4 Q8NF17 homo sapien

19 441 23.8 354 4 Q8ETT2 homo sapien

20 440.5 23.7 437 11 Q9R1A4 musculus

21 440 23.7 463 11 Q99LC4 musculus

22 440 23.7 469 11 Q8R3V9 musculus

23 421 22.7 473 11 Q9D8L4 musculus

24 402.5 21.7 679 4 Q96PQ8 homo sapien

25 399 21.5 468 11 Q99L31 musculus

26 399 21.5 473 11 Q99L25 musculus

27 398 21.4 470 11 Q7TMK1 musculus

28 395.5 21.3 473 11 Q9R3H6 musculus

29 395.5 21.3 474 11 Q96PQ8 homo sapien

30 377.5 20.0 492 4 Q7Z379 homo sapien

31 358 19.3 496 4 Q96KX8 homo sapien

32 359.5 19.9 416 4 Q9NPP5 homo sapien

33 360 19.4 493 4 Q8NCL6 homo sapien

34 359 19.3 404 4 Q9UP60 homo sapien

35 358 19.3 494 4 Q96K5B homo sapien

36 358 19.3 496 4 Q96KX8 homo sapien

37 358 19.3 497 4 Q8WY24 homo sapien

38 355.5 19.2 499 4 Q8N5K4 homo sapien

39 355 19.1 496 4 Q96D90 homo sapien

40 351.5 18.9 587 13 Q7T0R1 xenopus laevis

41 348 18.8 426 11 Q9DCD9 homo sapien

42 346 18.6 500 4 Q9BVO0 homo sapien

43 345 18.6 486 11 Q91Z07 homo sapien

44 345 18.6 487 11 Q99KA4 homo sapien

45 338.5 18.2 479 11 Q99M22 musculus

17 446 24.0 521 4 Q8N4Y9 homo sapien

18 444 23.9 509 4 Q8NF17 homo sapien

19 441 23.8 354 4 Q8ETT2 homo sapien

20 440.5 23.7 437 11 Q9R1A4 musculus

21 440 23.7 463 11 Q99LC4 musculus

22 440 23.7 469 11 Q8R3V9 musculus

23 421 22.7 473 11 Q9D8L4 musculus

24 402.5 21.7 679 4 Q96PQ8 homo sapien

25 399 21.5 468 11 Q99L31 musculus

26 399 21.5 473 11 Q99L25 musculus

27 398 21.4 470 11 Q7TMK1 musculus

28 395.5 21.3 473 11 Q9R3H6 musculus

29 395.5 21.3 474 11 Q96PQ8 homo sapien

30 377.5 20.0 492 4 Q7Z379 homo sapien

31 358 19.3 496 4 Q96KX8 homo sapien

32 359.5 19.9 416 4 Q9NPP5 homo sapien

33 360 19.4 493 4 Q8NCL6 homo sapien

34 359 19.3 404 4 Q9UP60 homo sapien

35 358 19.3 494 4 Q96K5B homo sapien

36 358 19.3 496 4 Q96KX8 homo sapien

37 358 19.3 497 4 Q8WY24 homo sapien

38 355.5 19.2 499 4 Q8N5K4 homo sapien

39 355 19.1 496 4 Q96D90 homo sapien

40 351.5 18.9 587 13 Q7T0R1 xenopus laevis

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17 446 24.0 521 4 Q8N4Y9 homo sapien

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19 441 23.8 354 4 Q8ETT2 homo sapien

20 440.5 23.7 437 11 Q9R1A4 musculus

21 440 23.7 463 11 Q99LC4 musculus

22 440 23.7 469 11 Q8R3V9 musculus

23 421 22.7 473 11 Q9D8L4 musculus

24 402.5 21.7 679 4 Q96PQ8 homo sapien

25 399 21.5 468 11 Q99L31 musculus

26 399 21.5 473 11 Q99L25 musculus

27 398 21.4 470 11 Q7TMK1 musculus

28 395.5 21.3 473 11 Q9R3H6 musculus

29 395.5 21.3 474 11 Q96PQ8 homo sapien

30 377.5 20.0 492 4 Q7Z379 homo sapien

31 358 19.3 496 4 Q96KX8 homo sapien

32 359.5 19.9 416 4 Q9NPP5 homo sapien

33 360 19.4 493 4 Q8NCL6 homo sapien

34 359 19.3 404 4 Q9UP60 homo sapien

35 358 19.3 494 4 Q96K5B homo sapien

36 358 19.3 496 4 Q96KX8 homo sapien

37 358 19.3 497 4 Q8WY24 homo sapien

38 355.5 19.2 499 4 Q8N5K4 homo sapien

39 355 19.1 496 4 Q96D90 homo sapien

40 351.5 18.9 587 13 Q7T0R1 xenopus laevis

41 348 18.8 426 11 Q9DCD9 homo sapien

42 346 18.6 500 4 Q9BVO0 homo sapien

43 345 18.6 486 11 Q91Z07 homo sapien

44 345 18.6 487 11 Q99KA4 homo sapien

45 338.5 18.2 479 11 Q99M22 musculus

17 446 24.0 521 4 Q8N4Y9 homo sapien

18 444 23.9 509 4 Q8NF17 homo sapien

19 441 23.8 354 4 Q8ETT2 homo sapien

20 440.5 23.7 437 11 Q9R1A4 musculus

21 440 23.7 463 11 Q99LC4 musculus

22 440 23.7 469 11 Q8R3V9 musculus

23 421 22.7 473 11 Q9D8L4 musculus

24 402.5 21.7 679 4 Q96PQ8 homo sapien

25 399 21.5 468 11 Q99L31 musculus

26 399 21.5 473 11 Q99L25 musculus

27 398 21.4 470 11 Q7TMK1 musculus

28 395.5 21.3 473 11 Q9R3H6 musculus

29 395.5 21.3 474 11 Q96PQ8 homo sapien

30 377.5 20.0 492 4 Q7Z379 homo sapien

31 358 19.3 496 4 Q96KX8 homo sapien

32 359.5 19.9 416 4 Q9NPP5 homo sapien

33 360 19.4 493 4 Q8NCL6 homo sapien

34 359 19.3 404 4 Q9UP60 homo sapien

35 358 19.3 494

QY	23 PTYKLFHSSCPRGDAHSTIQOLCLVSGSPAKVHWT---LVDQEARLFPTYTRPK 78
Db	6 PKVFAALPGCGRTSD---STVALGCLVSGFPEPVKVSNSLNSG---VHTFPSVL-- 57
QY	79 REGQPSLQSEVNITQGOMMSNTYTCVKENGSTFE-----DSSRKCADSN--P 127
Db	58 -QSGGPVSLSSMVTVBASTW-TSETVTCNVAHSANFKVDRKIEPDPDNHOKVCDMSKP 115
QY	128 R-----GVSAYLSPSPD-LFTRKSPITCLVWDLAPSKGTVNLTVSASGKPVH 178
Db	116 KCPAPELIGGSVFLPPNPKDTLMTRPEVTCVVDVDSQENPDVKFWMYDGVETIA 175
QY	179 STRKEEIKQNGTITVSTLPGTRDNEGETIQCRVTHPILPRLMRSTTLPKGKLAPE 238
Db	142 VSVSPASTKGSVPLPCKRSSTSESTAAALCLVQDFPPEPVTVNSGALTSQ--VHT 198
QY	71 FPTYTRPKREGGOTFSLOSEVNITQGOMMSNTYTCVKENGSTFEDSSRKCADSN--P 127
Db	199 FPAVL---QSGGPVSLSSMVTVBASTW-LGKTVYCNVDRKIEPDPDNHOKVCDMSKP 123
QY	128 -----RGVSAVLRSRSPF-LFIRKSPITCLVWDLAPSKGTVNLTVSASGKPVH 178
RESULT 2	
Q8TC63	PRELIMINARY; PRT; 473 AA.
ID	Q8TC63; AC Q8TC63; DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo. [1]
OX	NCBI_TaxID=9606;
RP	SEQUENCE FROM N. A.
RN	NCBI_TaxID=10090;
RP	SEQUENCE FROM N. A.
RC	STRAIN=CS7BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX	Medline=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauser R.D., Collins J.S., Wagner L., Shearer C.M., Schuler G.D., Altshull S.F., Zeeberg B.R., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang T., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiriki S., Carninci P., Prange C., Raha S.S., Loquaiello N.A., Peters G.J., Abramson D., Mullahy S.J., Bosak S.A., McLean P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia J., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Soedergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Maddan A., Young A.C., Shlyvchenko I., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [2]
RN	SEQUENCE FROM N. A.
RC	STRAIN=CS7BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA	Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC025985; AAH25985.1; -;
GO	GO:0005507; F: copper ion binding; IEA.
DR	GO: GO:005489; F: electron transporter activity; IEA.
GO	GO:0006118; P: electron transport; IEA.
DR	InterPro; IPR00923; Bluetu1.
DR	InterPro; IPR00710; Ig-like.
DR	InterPro; IPR00306; Ig_Mic.
DR	InterPro; IPR00596; Ig_v.
PFAM	PF000497; Ig; 4.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS00196; COPPER_BLUE; 1.
DR	PROSITE; PS05083; Ig_Like; 4.
DR	InterPro; IPR00306; Ig_Mic.
DR	InterPro; IPR00596; Ig_v.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS00196; COPPER_BLUE; 1.
DR	PROSITE; PS05083; Ig_Like; 4.
KW	Hypothetical protein.
SQ	SEQUENCE 473 AA; 51986 MW; B29920B09BA369F5 CRC64;
Query Match	25.8%; Score 479.5; DB 4; Length 473; Best Local Similarity 34.9%; Pred. No. 1.2e-55; Matches 120; Conservative 62; Mismatches 129; Indels 33; Gaps 11;
QY	18 VILIPPTW--LHFSSCPRGDAHSTIQOLCLVSGSPAKVHWT---LVDQEARL 70
Db	142 VSVSPASTKGSVPLPCKRSSTSESTAAALCLVQDFPPEPVTVNSGALTSQ--VHT 198
QY	71 FPTYTRPKREGGOTFSLOSEVNITQGOMMSNTYTCVKENGSTFEDSSRKCADSN--P 127
Db	199 FPAVL---QSGGPVSLSSMVTVBASTW-LGKTVYCNVDRKIEPDPDNHOKVCDMSKP 123
QY	128 -----RGVSAVLRSRSPF-LFIRKSPITCLVWDLAPSKGTVNLTVSASGKPVH 178
RESULT 3	
Q7MT6	PRELIMINARY; PRT; 614 AA.
ID	Q7MT6; AC Q7MT6; DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)
DE	Hypothetical protein.
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurgnathi; Muridae; Murinae; Mus. [1]
OX	NCBI_TaxID=10090;
RP	SEQUENCE FROM N. A.
RC	STRAIN=CS7BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX	Medline=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauser R.D., Collins J.S., Wagner L., Shearer C.M., Schuler G.D., Altshull S.F., Zeeberg B.R., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang T., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiriki S., Carninci P., Prange C., Raha S.S., Loquaiello N.A., Peters G.J., Abramson D., Mullahy S.J., Bosak S.A., McLean P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia J., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Soedergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Maddan A., Young A.C., Shlyvchenko I., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [2]
RN	SEQUENCE FROM N. A.
RC	STRAIN=CS7BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA	Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC053409; AAH54409.1; -;
KW	Hypothetical protein.
SQ	SEQUENCE 614 AA; 67746 MW; 839BAF3BB0124F89 CRC64;
Query Match	25.3%; Score 470; DB 11; Length 614; Best Local Similarity 34.1%; Pred. No. 1.3e-34; Matches 112; Conservative 57; Mismatches 139; Indels 20; Gaps 9;
QY	23 PTYKLFHSSCPRGDAHSTIQOLCLVSGSPAKVHWT---LVDQEARL 70
Db	250 PNNTV-----VPRDFGSGPAPSKLCKIACETNTPPEPVTVNSGALTSQ--VHT 198
QY	76 RPKREGGOTFSLOSEVNITQGOMMSNTYTCVKENGSTFEDSSRKCADSNPRGVAYL 134
Db	307 ENKGSTQTYKVISETLSEIDWLNINWVTCRVDHGLTFLKVNSTCAASPTILFT 366
QY	135 SRSPPFDFIRKSPITCLVWDLAPSKGTVNLTVSASGKPVH 194

RESULT 4

OBVCX7 PRELIMINARY; PRT; 613 AA.

OBVCX7, 01-MAR-2-2002 (TREMBrel. 20, Created)

DT 01-MAR-2-2002 (TREMBrel. 20, Last sequence update)

DT 01-OCT-2-2003 (TREMBrel. 25, Last annotation update)

DE HYPothetical protein.

GN IGH-6.

OS Mus musculus (Mouse)

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Salivary Gland;

RA Strauberg R.

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC01315; AAH8315.1; -.

DR MGI; MGI-96448; IgH-5

DR InterPro; IPR00110; Ig-like.

DR InterPro; IPR003596; Ig MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 5.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 5.

DR PROSITE; PS00290; Ig_MHC; 3.

DR PROSITE; PS00290; Ig_MHC; 3.

KW Hypothetical protein

SQ SEQUENCE 613 AA;

Query Match 25.3%; Score 469; DB 11; Length 613; Best Local Similarity 34.1%; Pred. No. 1. 1e-34; Matches 112; Conservative 139; Indels 20; Gaps 9;

QY 23 PTYKLFHSSCDPR---GDAHSTIQIQLCLVSGFSPAKVHVLVLDGQEAENLF---PYTT 75

Db 249 PNVNUP--VPPRGPGFSPGPPAKPSKSLICAEATNPKPTPPTVSYWLKQKLVSGFTDPVTT 305

QY 76 RPKREGGOTFSQLESEVNTTQGOMMSNTYCHVKNGSIF-EDSSPKCALSNPREVASYI 134

Db 306 ENKGSTFQTKVISTLITISIDWLNINVTCYDHLGLTFLKVNVSSTCASPSTDILTT 365

QY 135 SRSPSPFLFIRKSPPTICLWDLAPSKGTVLWTWSRASKGKVNHSRKKEKQKGTLTT 194

Db 366 IPSPFADIFLSSLSANLITVLSNLTAYE-TINISWASQSGEPLETKIKMPSHNGPTSAK 424

QY 195 STLPVGGRDWIGEETYCCRVTPHPLBAMSTTKPGK--RLAPVYMPMPPSPETG-- 250

Db 425 GVASVCFEDWNRKEFVCTVTHDLPSQKPKFISK-PNEVHKHPPAVVLPARQINLR 483

QY 251 TPTVTCLRGYPSSESVQWLFNNEEDHTGHTTTRPQKHDGTPSPFFYPSRMLVNGI 310

Db 484 ESAVUTCLVKGFSPADISVOMLQRGQLPQEKVTSAPMPERPGCPGPFYHSLTVTEB 543

QY 311 WEKGNLTVCRVHEALP--SRTLEKS 335

Db 544 WNSGETVTCVVSHALPHVUTERTVDKS 571

RESULT 5

OBWXT1 PRELIMINARY; PRT; 375 AA.

OBWXT1, 01-JUN-2003 (TREMBrel. 24, Created)

OBWXT1, 01-JUN-2003 (TREMBrel. 24, Last sequence update)

OBWXT1, 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DB Human full-length cDNA clone CSODD006YL02 of neuroblastoma of Homo sapiens (Human).

OS Homo sapiens (Human).

OC Eukaryota; Metacoz; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Neuroblastoma;

RA Genoscope;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RT [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Neuroblastoma;

RA Li, W.B.; Gruber, C.; Jesse, J.; Polaxes, D.; "Full-length cDNA libraries and normalization;" Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BA16120; CAD61894.1; -.

DR GO; GO:0046221; C:extrachromosomal DNA; IEA.

DR InterPro; IPR00710; Ig-1 like.

DR InterPro; IPR03597; Ig_C1.

DR InterPro; IPR00006; Ig_MHC.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00407; IgC1; 3.

DR PROSITE; PS50835; Ig_LIKE; 3.

DR PROSITE; PS00290; Ig_MHC; 3.

KW Plasmid

SQ SEQUENCE 375 AA; 41272 NW; TACD1AF4399C5EEB CRC64;

Query Match 25.1%; Score 465; DB 4; Length 375; Best Local Similarity 31.1%; Pred. No. 1. 9e-34; Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

QY 17 PVTIIT---PPTVLFPHSCDPR---GDAHSTIQIQLCLVSGFSPAKVHVLVLDGQEAEN 69

Db 24 PLPVTAELPPKVSVF--VPPRGPGFENPRKS-KLICQATGSPRSQPROQVSNLREGKQVG 79

QY 70 LPVTT---RPKREGGOTFSQLESEVNTTQGOMMSNTYCHVKNGSIF-EDSSPKCA 123

Db 80 --GVTVOAERAKESQPTVKTSTIKSWSLQSMFTCRVDRHGLTQONASSMC 137

QY 124 DSNPRGVAYLRSPPFDLPIRKSPPTICLWDLAPSKGTVLWTWSRASKGKVNHSRKKE 183

Db 138 PDQDTATRVPATPPSPASIFPTKSTKTCVWLT-TYDSTVSWPPTQNGEAVKHTN 196

QY 184 EKORNGTHTVTSIPLVPGFDRWTEGETVYQCRVTPHPLBAMSTTKPGKRL-APEVYML 242

Db 197 ESHPNATSAVGASBASICEDDWSNGERTCTVTHDLSPLKOTISKPKGVHLRPDVYLL 256

QY 243 PPEPETG--TPTVTCLRGYPSSESVQWLFNNEEDHTGHTTTRPQKHDGTPSPFFYPS 300

Db 257 PPARKQNLRESATVPTVTSIPLVPGFDRWTEGETVYQCRVTPHPLBAMSTTKPGKRL-APEVYML 316

QY 301 YSMVLYNLSIWEKGNLTVCRVHEALP--SRTLEKS 335

Db 317 HSILTVSEBEMNTGETTCVVVAHEALPNRVUTERTVDKS 354

RESULT 6

OBWXT4 PRELIMINARY; PRT; 588 AA.

OBWXT4, 01-MAR-2002 (TREMBrel. 20, Created)

DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DR Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC01235; AAH1235.1; -.
 DR InterPro; IPR00710; Ig-like.
 DR InterPro; IPR03006; Ig_MEC.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; Igv_1.
 DR PROSITE; PSS0835; Ig_LIKE_5.
 DR PROSITE; PS00290; Ig_MHC_3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65274 MW; 2DARFBFB7E055851 CRC64;

Query Match 25.1%; Score 465; DB 4; Length 597;
 Best Local Similarity 31.1%; Pred. No. 3. 5e-34; Indels 26; Gaps 11;
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

OY 17 PVVIL--PPTVLFPHSSCDPR---GDAHSTIQOLCLVLGSFSPAKVHVTWLGQEAEN 69
 Db 246 PLVIAELPPKVSVF--VPPRDGFGRNPRKS-KLICQATFSPROIOWLRECKQVG 301

OY 70 LFVTT---RPKREGQTSQLESEWNTIQQWMSNTYCHVKHNGSIF-EDSSRKCA 123
 Db 360 PDDDTAAKRVFAIPPSFSPLFLKSPTRKTSKTLCLVDTL-TYDSTVISMWIRQNGAVKHTNIS 359

OY 184 EKRGNGTIVTSLPVGTRDMEGETYQCRVTHPHRPLAHLRSTKLPGRK-APEVYML 242
 Db 419 ESHNATSAVABASICEDDNNSGERFTCTVHTDLSPLQKOTSRPKGVYALHRPDVYLL 478

OY 243 PPSPEETG--TTRTVLGLRGYPSSETSVQLENFNEEDHTQHTTRPQDHGTPSFFL 300
 Db 479 PPARQNLRESATITCLVGTGFSPADMFMQGQPLSPKVKVTSAPMPEPQAPGRYFA 538

OY 301 YSRMLVNUKSIWEKGNLVTCRVVHEALPG--SRTLEKS 335
 Db 539 HSILTVSEEMNTGETTCVVAHEALPENRVTVDKS 576

Db

RESULT 7

O9BUL0 PRELIMINARY; PRT; 597 AA.
 ID O9BUL0 PRELIMINARY; PRT; 597 AA.
 AC O9BUL0_17_2001 (TREMBrel. 17, Created)
 AC O9BUL0_01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Metacora; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC TISSUE=Muscle, and Lymph;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006180; AAH06180.1; -.
 DR EMBL; BC0061872; AAH061872.1; -.
 DR RSPB; P01825; 7FAB.
 DR InterPro; IPR00710; Ig-like.
 DR InterPro; IPR03006; Ig_MEC.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; Igv_1.
 DR PROSITE; PSS0835; Ig_LIKE_5.
 DR PROSITE; PS00290; Ig_MHC_3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65300 MW; 2DAPAD50A6375851 CRC64;

Query Match 25.1%; Score 465; DB 4; Length 597;
 Best Local Similarity 31.1%; Pred. No. 3. 5e-34; Indels 26; Gaps 11;
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

OY 17 PVVIL--PPTVLFPHSSCDPR---GDAHSTIQOLCLVLGSFSPAKVHVTWLGQEAEN 69
 Db 246 PLVIAELPPKVSVF--VPPRDGFGRNPRKS-KLICQATFSPROIOWLRECKQVG 301

QY 70 LFPYTT---RKPREGGOTFSLOSEVNITQGOMSSNTYCHKHNSIF-EDSSRKCA 123
 302 --GVTIDQVQAEAKESGPTVKTIVSTLTKESDMLQSMTFCDRHGILTFOQNAASSCV 359
 QY 124 DSNPRGVASVLSRSPSPFDLFIKSPTITCULVLDAPSKEGVNLUTWSRASKPVNHSKRE 183
 360 PDQDTAIRVRAIPPSFASIFTKSTKLTICLVTDLT-TVSNTISWTRONGEAVKHTNIS 418
 QY 184 EKQRGTLTIVSTLPGTWDWIEBPTVQCRVTHPLPMLRSTIKLCKRL-APEVNL 242
 419 ESHPNATSAVGEASICEDDWNSSERFTCTVTHPLSPKQTSRPGVALHRPDVYL 478
 Db 243 PPSBETG--TTRTVCILRGFVSEISVQWLFNNEBDHTGHITTRQKDGTDPSSFL 300
 QY 479 PPABOLNLRBESATITCULVGFSPADVFVQWMORGQPLSPEKVTISAMPEQAFGRYFA 538
 QY 301 YSRMLVNSKSTWEKGMLVTCWHEALPG---SRITLEKS 335
 539 HSILTVSEBNTGTYTCVVAHELPNRVTERIVDKS 576

RESULT 9
 Q96B9 PRELIMINARY; PRT; 597 AA.
 AC 096B9 ID 096B9
 DT 01-DEC-2001 (TREMBirel. 19, Created)
 DT 01-DEC-2001 (TREMBirel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBirel. 25, Last annotation update)
 DE Hypothetical protein.
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strauberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AACN1857.1; -.
 DR PIR; S15590; S15590.
 DR InterPro; IPR0070; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF0047; Ig_5.
 DR SMART; SM0406; IgV_1.
 DR PROSITE; PS5035; Ig_LIKE; 5.
 DR PROSITE; PS00290; Ig_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
 Query Match 25.1%; Score 465; DB 4; Length 613;
 Best Local Similarity 31.1%; Pred. No. 3.7-34;
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

QY 17 PVTIIL---PPTVKLFHSCDPR---GDAHSTIQLCLVGSFSPAKVHTWLVQGELEN 69
 Db 241 PLPVIAELPPKVSVF---VPRDGFGNFRKS-KLICATGFSPROQVSWIREKGKQGS 296
 QY 70 LFPYTT---RKPREGGOTFSLOSEVNITQGOMSSNTYCHKHNSIF-EDSSRKCA 123
 Db 297 --GVTIDQVQAEAKESGPTVKTIVSTLTKESDMLQSMTFCDRHGILTFOQNAASSCV 354
 QY 124 DSNPRGVASVLSRSPSPFDLFIKSPTITCULVLDAPSKEGVNLUTWSRASKPVNHSKRE 183
 Db 355 PDQDTAIRVRAIPPSFASIFTKSTKLTICLVTDLT-TVSNTISWTRONGEAVKHTNIS 413
 QY 184 EKQRGTLTIVSTLPGTWDWIEBPTVQCRVTHPLPMLRSTIKLCKRL-APEVNL 242
 Db 414 ESHPNATSAVGEASICEDDWNSSERFTCTVTHPLSPKQTSRPGVALHRPDVYL 473
 QY 243 PPSBETG--TTRTVCILRGFVSEISVQWLFNNEBDHTGHITTRQKDGTDPSSFL 300
 Db 474 PPABOLNLRBESATITCULVGFSPADVFVQWMORGQPLSPEKVTISAMPEQAFGRYFA 533
 QY 301 YSRMLVNSKSTWEKGMLVTCWHEALPG---SRITLEKS 335
 Db 534 HSILTVSEBNTGTYTCVVAHELPNRVTERIVDKS 571

RESULT 11
 Q8WUKL ID Q8WUKL
 Q8WUKL PRELIMINARY; PRT; 613 AA.
 AC Q8WUKL;
 DR 01-MAR-2002 (TREMBirel. 20, Created)
 DR 01-MAR-2002 (TREMBirel. 20, Last sequence update)
 DR 01-OCT-2003 (TREMBirel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).

QY 301 YSRMLVNSKSTWEKGMLVTCWHEALPG---SRITLEKS 335
 539 HSILTVSEBNTGTYTCVVAHELPNRVTERIVDKS 576

RESULT 10
 Q96EY0 ID Q96EY0
 AC 096EY0
 DT 01-DEC-2001 (TREMBirel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBirel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strauberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AACN1857.1; -.
 DR PIR; S15590; S15590.
 DR InterPro; IPR0070; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF0047; Ig_5.
 DR SMART; SM0406; IgV_1.
 DR PROSITE; PS5035; Ig_LIKE; 5.
 DR PROSITE; PS00290; Ig_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Matches	116;	Conservative	63;	Mismatches	132;	Indels	36;	Gaps	12;
Qy	18	VTLIPPTVY--LFHSSCDPREGDAHSTIQLCLVSGPSPAKHWTW---LVDQEAENL							70
Db	136	VTVSSASTKPSVPLAPSSKSTSGTAAGCLQYFPRPVTSWNGLATSG--VHT							192
Qy	71	FPYTRPKREGQTSLSQSEVNITOCQWMSNTTCHVKGNS-TFE-----DSSR							120
Db	193	FPAVL---QSSGLYLSLSVTVSSS-LGTOVYICNUHKPSNTKVKKVSPKSCDKTH							247
Qy	121	KC---ADSPRPGVSAVLSPPSPFD-LFIRKSPITCLVVDLAPSKGTWNLWRSRASKP							175
Db	248	TCPGPAPELIGGPSTELPPKPKOTIMSRTPVTCVWVWDVSHEDPEYKFWYDGEV							307
Qy	176	VNHSTRKEEKQNGTILTIVTSLPVGTRDWEGETYQCRVTPHPLPRAMLRSTMKLPGKRL							235
Db	308	HNAKTKPREEQINSTYRVVSVLTVLHQDWIANGKEYKCKISNKALPAPETKISKAGKPR							367
Qy	236	APEVYMLPPRSPPE--TGTRTRWTCILRGPFYSEIYQWLNENRDEHTGHITTRPQDKHGT							294
Db	368	EPQVTLPPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGOPEN--NIKTPPVLD--S							423
Qy	295	DPSFTLYSRMLVNLKSIWEKNTLVICRVWHEALPESRTLKSAYHSG							341
Db	424	DGSFFFLYSKUTVDKSRWQCNVFSCSVMHALHNHYT-QKSLSLSPG							469

Search completed: February 26, 2004, 12:00:53
 Job time : 48 secs

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Rattus*.
 OX NCBI_TaxID=10116;
 RP [1] SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
 RC STRAIN=LOUIC/WSL;
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Patterson U., Engstrom A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 E";
 RL Nucleic Acids Res. 10:6041-6049(1982).
 RN [2] SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
 RP SEQENCE OF 205-306 FROM N.A.
 RX MEDLINE=83182019; PubMed=680340;
 RA Kindsvogel W.R., Reddy E.B., Moore J.M., Faust C.H. Jr.;
 RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
 construction, identification, and DNA sequence.;"
 RL DNA 1-335-343 (1982).
 RN [3] SEQUENCE OF 205-306 FROM N.A.
 RX MEDLINE=82174576; PubMed=680338;
 RA Hellman L., Pettersson U., Bennich H.;
 RT "Characterization and molecular cloning of the mRNA for the heavy
 (epsilon) chain of rat immunoglobulin E";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
 CC !- SIMILARITY: Contains 4 immunoglobulin-like domains.
 CC
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 CC
 CC
 DR EMBL; J00744; AAA4139.1; ALT INIT.
 DR PIR: A93442; ERT.
 DR HSSP; P01854;
 DR InterPro; IPR00110; IgE.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 4.
 DR PROSITE; PS00835; Ig_LIKE; 4.
 DR PROSITE; PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
 FT NON_TER 1
 FT DOMAIN 5 89
 FT DOMAIN 103 201
 FT DOMAIN 205 305
 FT DOMAIN 314 414
 FT DOMAIN 168 308
 FT CONFLICT R -> N (IN REF. 2).
 FT CONFLICT R -> L (IN REF. 2).
 SO SEQUENCE 429 AA; 48671 MW; D2970B34EF8A7B0 CRC64;
 Query Match 41.4%; Score 767.5; DB 1; Length 429;
 Best Local Similarity 45.8%; Pred. No. 1.1e-51; Gaps 4;
 Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 4;
 OY 17 PVMIPPPVKKPHSSCDPQRGDAHSTQQLICLVSFGSPAKVWTWVLDGQARENLEPYTR 76
 DB 97 PPNIKTQVTDLHSSCDPNA FHSIQVLYQVHQNDMSIHWLMDRKI----YETH 150
 OY 77 PK---RBBGGOPPSLQSEVNITQGQWNSNTYTCRKHNSIFEDSSRKADSNSRQVA 132
 DB 151 AGNLIKEGKLASTYSLRINTQOQMSSESTICKVQSOQENYWAHTRRCSDEPRGVIT 210
 OY 133 YLSRSPSPDFLFLRKSPPTCIVDQPLSKGTVLNTWSRAGKPKVHSTRGEKQNGTIT 192
 DB 211 VLPSPSPDLYENGTPKLCLVIDL-ESENNTIVWTRRCKSISASQSTKHNRAT 269
 OY 193 VTSILPQGTRDWEGETYQCRVTHPLRMLRMSTKLPSKGLRAEVMPPSPSPETGTT 252
 DB 270 ITSLIPVDAKDVIEGEGVQCRVTHPLRMLRMSTKLPSKGLRAEVMPPSPSPETGTT 329

RESULT 3

QY 253 RTVCLCLGFPYRSISYQWLFNNEEDHTGHHTTRPQDKHDGTPSPFLYSLVNUKSIWE 312
 ID EPC_MOUSE STANDARD; PRT; 421 AA.
 AC P06736; P01856;
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig epsilon chain C region.
 OS Mus musculus (Mouse).
 OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=84226092; PubMed=6329728;
 RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
 RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
 comparison with the human epsilon gene sequence.;"
 RL EMBL; J. 1:1117-1123 (1982).
 RN [2] SEQUENCE FROM N.A.
 RX MEDLINE=8311774; PubMed=6818533;
 RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
 RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
 chain cDNA.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856 (1982).
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X01857; CA25977.1; -;
 DR EMBL; X01857; CA25978.1; -;
 DR PIR; A00144; ERMSS.
 DR PIR; A00145; ERMSS.
 DR HSSP; P01854; IgE.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS00835; Ig_LIKE; 4.
 DR PROSITE; PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DOMAIN 1 90 CH1.
 FT DOMAIN 91 197 CH2.
 FT DOMAIN 198 304 CH3.
 FT DOMAIN 305 421 CH4.
 FT DISULFID 23 75 BY SIMILARITY.
 FT DISULFID 121 180 BY SIMILARITY.
 FT DISULFID 226 285 BY SIMILARITY.
 FT DISULFID 330 392 BY SIMILARITY.
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 84 Score 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 421 AA; 47320 MW; 899981F30A06B47 CRC64;

Best local Similarity 40.5%; Score 751; DB 1; Length 421;
 Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;

QY 2 FHHHHHHHTSLPES---GPVITIPPTVLETSQCDRGDASTIQCLVSGFSPKV 56
 Db 73 FTCHVTHPPSFNESTRTILVRPVNITEPTTLELHSSCDPNA-FHSTIQLCFTYGHILNDV 131

QY 57 HVTMNDGEEAENIIPYITPRKGQTSLSQWNIQGQMSNTTCHWKGNSIFE 116
 Db 132 SVSHMMDRDTDTLAQTVLKEE-GKLASTCSKLNTBQWNSESTPCKVTSQGVNL 190

QY 117 DSSRKCADSNPRGYSAYLSRSPFDLFIKSPTTICLVDLASSKGTVNLWSRASGV 176
 Db 191 AHTRRCPDPHEPRGVITYLIPSPDLYQNGAPKLTCLVLDLESK-NYAVTWQEKCTSV 249

QY 177 NHSTREEKEKONGTITVTSPLVPGTRDWTIEGETTQCRVTHPHPLRALKMSTTKLPGKLA 236
 Db 250 SASQWYKHNNTSITSLPVWAKDNEGGYCYCTVNHDPDPPKPTVRSITKPPGQRSA 309

QY 237 PEVVLPPSPBETGTTVTCILGFGYFSEBISVWLFNNEBEDHTGHHTTRPQDGDTP 296
 Db 310 PEVVFPPPPSEEDSKRITCLQNPFDISVQWLGDKLNSQHSTTPKNSNGQ 369

QY 297 SFFYLSRMVNLNSKTIWEKGMLVTCRVHPEALPGSTTEKSLHYSAGN 342
 Db 370 GFTTSEERVAKTIVTORKTQVHAEALQPKWERTISTSGN 415

RESULT 4
 MUCM_RABBIT STANDARD: PRT: 479 AA.
 ID MUCM_RABBIT
 AC P04221;
 DT 20-MAR-1997 (Rel. 04, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig mu chain C region membrane bound form.
 OS Oryctolagus cuniculus (Rabbit).
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN NCBI_TaxID=9986;
 RP SEQUENCE FROM N.A. (A2 ALLOTYPE).
 RX MEDLINE-8408930, PubMed=6418803, Bernstein K.E., Alexander C.B., Reddy B.P., Mage R.G.;
 "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of VHA2 allotype: comparisons with VHA1 and membrane mu sequences.";
 J. Immunol. 132:490-495 (1984).
 CC -1- ALTERNATIVE PRODUCTS:
 CC - Event=Alternative splicing; Named isoforms=2;
 CC Comment=During differentiation, B lymphocytes switch from expression of isoform Membrane-bound to isoform Secreted;
 CC Name=Membrane-bound;
 CC IsoId=P04221-1; Sequence=Displayed;
 CC Name=Secreted;
 CC IsoId=P04221-1; Sequence=External;

QY 5 HHTHHTSLPESGV-TIIPPTVLFHSSCDR---GDAHSTIQCLVSGFSPKVHT 59
 Db 94 HENSNRDLRVSPTVPSDLSLPPNTSVS-IPPRDSFGSGCTRSRLLCOATGSPKQISVS 150

QY 60 WLVDQGEAEN---LFPPTTRPREGGTFSLSQSEVNITQGQMSNTTCHWKGNSIFE 116
 Db 151 WWDQGQKVEGWLTKPVAETTGAGPATPSLSSMLTIDESLQSLPTCVDHGRFED 210

QY 117 DSSRKCADSNPRGYSAYLSRSPFDLFIKSPTTICLVDLASSKGTVNLWSRASGV 173
 Db 211 KNTMSMSEGSTTSPGQVFPPIAPSADTFLSKSARLCLVTDIT-TYGSNISWASHG 269

QY 174 KPNHSTREEKEKONGTITVTSPLVPGTRDWTIEGETTQCRVTHPHPLRALKMSTTKLPGK 233
 Db 270 KALDTHMNTESHPNATPSAMGEASVCAEDWNSGEGPCTVTHADLPPKTTISK--SR 327

QY 234 RLA---SEVYMPSPSPS--TGTTRTTCILGFGYFSEBISVWLFNNEBEDHTGHHTTRP 288
 Db 328 EVAKHPVAVVPPAROLVLEBESATVCLVKGFSADFWVWQORGQPLSSDKYTS 387

QY 289 QDQHGTSPSFYFSRMVNLNSKTIWEKGMLVTCRVHPEALPGSTTEKSLHYSAG 341
 Db 388 APPOAQLYFTHSTLTVEDDNSGTPTCVGHEALPHMVTERTVDKSTIEGEGV 443

RESULT 5
 MTC_RABBIT STANDARD: PRT: 458 AA.
 ID MTC_RABBIT
 AC P03988;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig mu chain C region secreted form.
 OS Oryctolagus cuniculus (Rabbit).
 CC Fukukawa, Maruya, Chouraki, Granata, Vartakarata, Ruljelecamoni
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RL Mol. Immunol. 16:923-925 (1979).
 RN [7] REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T.; Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8] SEQUENCE OF 1-121 (DCT).
 RP MEDLINE:9525298; PubMed:7737190;
 RA Stoppini M.; Bellotti V.; Negri A.; Merlini G.; Garver F.; Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins."
 RL Bur. J. Biochem. 228:886-893(1995).
 RN [9] DISULFIDE BONDS.
 RP MEDLINE:72033500; PubMed=44940472;
 RA Milstein C.; Francione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10] DISULFIDE BONDS.
 RP MEDLINE:69064124; PubMed=5782707;
 RA Frangione B.; Milstein C.; Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 CC
 CC
 DR EMBL; J00230; AABE59393.1; -.
 DR PIR; A93056; G2HU.
 DR HSSP; P01857; G2HU.
 DR Genew; HGNC:5526; IGHG2.
 DR MIM; 147110; -.
 DR GO; GO:0005624; C_membrane_fraction; NAS.
 DR GO; GO:0003823; Part antigen binding; TAS.
 DR GO; GO:0005955; Immune response; NRS.
 DR InterPro; IPR00357; Ig_C1.
 DR InterPro; IPR00306; Ig_MHC.
 DR Pfam; PF00047; Ig_C1.
 DR SMART; SM00407; Ig_C1; 2.
 DR PROSITE; PS50835; Ig_LIKE; 3.
 DR PROSITE; PS00290; Ig_MHC; 2.
 DR KNN; NON_TER 1 1 Immunoglobulin domain; Immunoglobulin C region.
 PT DOMAIN 1 98 CH1.
 PT DOMAIN 99 110 HINGER.
 PT DOMAIN 111 219 CH2.
 PT DOMAIN 220 326 CH3.
 PT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 PT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 PT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 PT DISULFID 103 103 S -> A (IN MELIOMA PROTEINS T11 & ZIE).
 PT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 PT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 PT DISULFID 140 200
 PT DISULFID 246 304 AT OR NEAR THE COMPLEMENT-BINDING SITE.
 PT SITE 156 REMOVED POST-TRANSLATIONALLY (PROBABLE).
 PT MOD_RES 326 326 S -> A (IN MELIOMA PROTEINS T11 & ZIE).
 PT VARIANT 60 60 /Pfam=var_003889.
 PT CONFLICT 109 109 C -> S (IN REF. 3).
 SQ SEQUENCE 326 AA; 35884 MW; 8310878C678C9C CRC64;

Query Match 26.2%; Score 486.5; DB 1; Length 326;
 Best Local Similarity 36.2%; Pred. No. 2; e=8-10;
 Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;
 DISULFID 215

RESULT 7
 NUC_MESAU STANDARD; DRT; 454 AA.
 ID P06317; 1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DR 19 mu chain C region.
 OS *Mus musculus* (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC *Mus musculus*.
 RN [11] TAXID=10036;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE:85297761; PubMed=2394005;
 RA McGuire K.L.; Duncan W.R.; Tucker P.W.;
 RT "Phylogenetic conservation of immunoglobulin heavy chains: direct
 comparison of hamster and mouse Cm genes.";
 RL Nucleic Acids Res. 13:561-5628(1985).
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 CC
 DR EMBL; X02804; CA026574.1; -.
 DR HSSP; P01854; Ig_E.
 DR InterPro; IPR00710; Ig-Like.
 DR InterPro; IPR00357; Ig_C1.
 DR InterPro; IPR00306; Ig_MHC.
 DR Pfam; PF00047; Ig_C1.
 DR SMART; SM00407; Ig_C1; 2.
 DR PROSITE; PS50835; Ig_LIKE; 4.
 DR PROSITE; PS00290; Ig_MHC; 3.
 DR KNN; NON_TER 1 1 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 PT DOMAIN 1 105 CH1.
 PT DOMAIN 106 218 CH2.
 PT DOMAIN 219 324 CH3.
 PT DOMAIN 325 454 CH4.
 PT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
 PT DISULFID 27 88 BY SIMILARITY.
 PT DISULFID 135 198 BY SIMILARITY.
 PT DISULFID 215 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).

FT DISULFID 245 304 BY SIMILARITY.
 FT DISULFID 292 292 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 352 414 BY SIMILARITY.
 FT DISULFID 453 453 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 454 AA; 50196 MW; 4DA2134612BE1469 CRC64;

Query Match 26.0%; Score 483; DB 1; Length 454;
 Best Local Similarity 34.0%; Pred. No. 7.9e-30; Matches 119; Conservative 58; Mismatches 147; Indels 26; Gaps 10;

Qy 5 HHHHT --LSIPESGPVTLIPTVVKHSSCDP-RGDAHSTIQLICLVGSPAKHVTW 60 DR SM005624; C:membrane fraction; NAS.
 91 HGGNTNKKDRV-IPVWVTPVNPVSVFVPSRDAFSGAPRKSRLCEASNPSKQITYSW 149 DR GO-003823; F:antigen binding; TAS.
 DR GO-000655; F:immune response; MAS.

DR InterPro; IPR00110; Ig-like.
 DR InterPro; IPR00306; Ig_McC.
 DR Pfam; PF00047; IgC1.
 DR PROSITE; PS5035; Ig_LIKE_3.
 DR PROSITE; PS0290; Ig_MHC_2.
 DR KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.

Qy 61 LVDQEALNL --PYTTRKREGGOTPSQSEVNTQGOMSSTVTCVKRNGSIR 116 FT DOMAIN 1 98 CH1.
 150 LRDGKPVKGFTTEPVTPERDGSGRPTYKVISTLTTESDWLNLNVYVCRVDRHGLTFWK 209 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 Qy 117 DSSRKCADSNRGSVASYLRSRSPFDLFIKRSPTICLVVLDLAPSKGTVNLTWRSASKEV 176 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 210 NYSITCAASSTDQAFPIPSFGFLANSATLCLVNLIA-TYDINISWSSRSGPL 258 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 177 NHSTRKEKQRNGTLTWTSLPVGTRDWIGETVQCRVTHPLR--ALMRSSTTL 230 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 269 ETKTKLUTESHNGTFSASIGEANCVEDWDSKEFVCTVTHRLSPKKEFISPREMKI 328 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF2088TA CRC64;

Query Match 25.6%; Score 476; DB 1; Length 327;
 Best Local Similarity 35.8%; Pred. No. 1.8e-29; Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;

Qy 289 QKDHGTPSPFELYSRMLVNSIWEKGNLVCRWHEALP--GRTLERS 335 DR 35 RGDASHSTIQLICLVGSPAKHVTW--LVDQEALNLFPYTRKREGGOTPSQSE 90
 329 P----PAVQOPLAREBOLIREBASATVICHVKGFSPADIFVQWLRQGQPLSQDKVVTSA 383 DR 16 RSTSEPAATAGCIVKDVQFPPSEVTVWNSGALTSG--VHFPAVLI--QSSGLYSS 68

Qy 384 MREQPAHLYVTHSVTUTBEBNWNSGETYCVVGEHALPMTVTRVRS 433 DR

RESULT 8

GC4_HUMAN STANDARD; PRT; 327 AA.

ID GC4_HUMAN STANDARD; PRT; 327 AA.

AC P01861; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig gamma-4 chain C region.
 IGH4.

OS Homo sapiens (Human).

OC Bukarayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=3157104; PubMed=6299662;
 RT Elision J.W., Buxbaum J.N., Hood J.E.;
 "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.",
 DNA 1:11-18 (1981).

RN [2] SEQUENCE OF 1-30 AND 81-326.

RX MEDLINE=0207660; PubMed=4196699;
 RT Pink J.R.L.; Buttner S.H.; de Vries G.M.; Milstein C.;
 "Human immunoglobulin subclases. Partial amino acid sequence of the
 constant region of a gamma 4 chain.",
 R.L. Biochem. J. 117:33-47 (1970).

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CC EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A0933; G440.
 DR PDB; 1DQ; 16-SEP-98.
 DR Genew; HGNC-5528; IGHG4.
 DR MIM; 147130; --.
 DR GO; GO-0005624; C:membrane fraction; NAS.
 DR GO; GO-003823; F:antigen binding; TAS.
 DR GO; GO-000655; F:immune response; MAS.

DR InterPro; IPR00110; Ig_C1.
 DR InterPro; IPR00306; Ig_McC.
 DR Pfam; PF00047; IgC1.
 DR PROSITE; PS5035; Ig_LIKE_3.
 DR PROSITE; PS0290; Ig_MHC_2.
 DR KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.

Qy 91 VUNITQGOMMSNTVTCVKRNGSIFEDSSRKCADSNP--RGVAVLRSRSP 139 DR 69 VVPPRSS--LGKTYTVCNDPKHPSNTKVKRVEVKYGPCCPSCPAPBFLGGPSVLFPPK 127

Db 140 P0-LFTRKSPPTICLVVLDLAPSKGTVNLWRSASKP VHISTRKEKQRNGTLTWTSLP 198 DR 128 KDTIMISRTPEVTCVVDVSOEDPAVQFNWYDGVEVHNAKTKFREEQNSTYRVL 187

Qy 199 VGTDRWIGEGETYVCRVTHPLPRLMRSTKLPSKRLAEEVYMPSPB--TGTTRTVC 257 DR 188 VHQDMDNGKVKYCKVSKNGKPLSSLEKKTISKAKGSPRPPROYTIPPSQEMTKVNLTC 247

Db 258 LIRGFYPSSETSVQWLNENRDEHTGHTTTRPQKQHGTDSFPLYSRMLVNSIWEKGNLV 317 DR 248 LVKGFPYSDIAVEWNSQOPEN--NYKTTPVLD--SGSFLYSLRITVDSKSRWQEGNF 303

Qy 318 TCRVHHLPSRTLEKLYSAG 341 DR 304 SC5VHHLAHMYT-QKSLSLIG 326

OS Homo sapiens (Human).

RESULT 9

MUC_HUMAN STANDARD; PRT; 454 AA.

ID MUC_HUMAN STANDARD; PRT; 454 AA.

AC P01871; 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, last annotation update)

DB Ig mu chain C region.
 IGHM.

OC	PROSITE; PS02290; IG_MEC; 3.
Mammal;	Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	ImmunoGlobulin domain; Immunoglobulin C region; Glycoprotein;
RN	SEQUENCE OF 1-434 FROM N.A.
RN	Medline:9033450; PubMed=215996;
RN	RA Friedlander R.M.; Nussenzweig M.C.; Leder P.;
RN	RT "Complete nucleotide sequence of the membrane form of the human IgM heavy chain,";
RT	RT heavy chain,";
RL	Nucleic Acids Res. 18:4278-4278(1990).
RN	[12]
RP	SEQUENCE (WALDENSTROM'S MACROGLOBULIN GAL).
RX	Medline:7505123; PubMed=4803843;
RA	Watanaabe S.; Barnikol H.U.; Horn J.; Bertran J.; Hilschmann N.;
RT	RT "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.) II: the amino acid sequence of the H-chain (mu-type), subgroup H III. Architecture of the complete IgM-molecule,";
RT	RT Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN	[13]
RP	SEQUENCE (GAL).
RX	Medline:81066716; PubMed=6777162;
RA	Mihaesco E.; Barnikol-Watanaabe S.; Barnikol H.U.; Mihaesco C.; Hilschmann N.
RA	"The primary structure of the constant part of mu-chain-disease protein BOT,"
RL	Eur. J. Biochem. 111:275-286(1980).
RN	[41]
RP	SEQUENCE (WALDENSTROM'S OU) DISULFIDE BONDS, AND CARBOHYDRATES.
RX	Medline:7405511; PubMed=4742735;
RA	Putman F.W.; Floret C.; Shinoda T.; Shimizu A.;
RA	"Complete amino acid sequence of the Mu heavy chain of a human IgM
RT	RT immunoglobulin.,";
RL	Science 182:287-291(1973).
RN	[5]
RP	PARTIAL SEQUENCE FROM N.A.
RX	Medline:82059479; PubMed=677778;
RA	Rabbitts T.H.; Forster A.; Milstein C.P.;
RT	RT "Human immunoglobulin heavy chain genes: evolutionary comparisons of chain cDNA and mouse-human hybridomas.,";
RT	RT C mu, C delta, C gamma genes and associated switch sequences.,";
RL	Nucleic Acids Res. 9:4509-4524(1981).
RN	[6]
RP	SEQUENCE OF 299-387 AND 438-454 FROM N.A.
RX	DOLBY T.W.; Devuono J.; Croce C.M.;
RA	"Cloning and partial nucleotide sequence of human immunoglobulin mu RT chain cDNA and mouse-human hybridomas.,";
RT	RT Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).
RL	RL "-1- MISCELLANEOUS: All 4 combinations of the S/G and V/G polymorphisms at positions 192 and 216 have been observed in human mu chains.
CC	CC
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CC	CC
DR	EMBL; X7115; CAA4971_1; ALT SEQ.
DR	HSP; P1857; IFCI;
DR	Genew; HGNC:15541; IGHM.
DR	MMI; 147020;
DR	GlycoSuiteDB; P01871; "-
DR	GO; GO:0005624; C-membrane fraction; NAS.
DR	GO; GO:0003823; F-antigen binding; TAS.
DR	GO; GO:0006955; P-immune response; NAS.
DR	InterPro; IPR07110; Ig-like.
DR	InterPro; IPR03597; Ig_C1.
DR	InterPro; IPR03006; Ig_MHC.
DR	Pfam; PF00047; Ig; 4.
DR	SMART; SNO407; Ig_C1; 3.
DR	PROSITE; PS50835; Ig_LIKE; 4.
RESULT 10	
MUC_MOUSE	
ID MUC_MOUSE	STANDARD;
AC P01872;	PRT; 455 AA.
DT 21-JUL-1986 (Rel. 01, Created)	
DT 21-JUL-1986 (Rel. 01, Last sequence update)	
DT 10-OCT-2003 (Rel. 42, Last annotation update)	
DB Ig mu chain C region, secreted form.	
OS Mus musculus (Mouse)	
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI_TaxID=10090;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX Medline:8106590; PubMed=6255422;	

RA Kawakami T., Takahashi N., Horio T.;
 RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and
 RT comparison with other immunoglobulin heavy chain genes.;"
 RL Nucleic Acids Res. 8:3933-3945(1980).
 [2]
 RN SEQUENCE FROM N.A.
 RP
 RX MEDLINE=82051295; PubMed=6795090;
 RA Goldberg G.I., Vann E.F., Zrolka A.M., Blattner F.R.;
 RT "Sequence of the gene for the constant region of the mu chain of
 RT Balb/C mouse immunoglobulin.;"
 Gene 15:33-42(1981).
 [3]
 RN SEQUENCE FROM N.A. (MYELOMA TPERC183).
 MEDLINE=81165562; PubMed=6260591;
 RA Auffray C., Rongeon F.;
 RT "Nucleotide sequence of a cloned cDNA corresponding to secreted mu
 RT chain of mouse immunoglobulin.;"
 RL Gene 12:77-86(1980).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
 RX MEDLINE=79223904; PubMed=11247;
 RA Kehry M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hood L.E.,
 RT "Amino acid sequence of a mouse immunoglobulin mu chain.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
 RN [5]
 RP REVISION (MOPC 104E).
 RX MEDLINE=8305344; PubMed=6816276;
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains.;"
 RL Biochemistry 21:5415-5424(1982).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Name=isoforms=2;
 CC Comment="During differentiation, B lymphocytes switch from
 CC expression of isoform Membrane-bound to isoform Secreted;
 CC Name=Secreted;
 CC IsoID=P01872-1; Sequence=Displayed;
 CC Name=Membrane-bound;
 CC IsoID=P01873-1; Sequence=External;
 CC
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 CC
 DR EMBL; V00827; -; NOT_ANNOTATED_CDS.
 DR PIR; A02166; MIM5.
 DR HSSP; P01857; IFC1.
 DR InterPro; IPR00110; Ig-like.
 DR InterPro; IPR003597; Ig CL.
 DR InterPro; IPR003006; Ig_MEC.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00407; IgC1_2.
 DR PROSITE; PS50835; Ig_LIKE_4.
 DR PROSITE; PS00290; Ig_MHC_3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1
 DOMAIN 1 105 CH1.
 FT DOMAIN 106 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DOMAIN 325 436 CH4.
 FT DOMAIN 437 455 C-TERMINAL SEGMENT OF SECRETED FORM.
 FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
 FT DISULFID 28 89 BY SIMILARITY.
 FT DISULFID 136 199 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 216 305 BY SIMILARITY.

RESULT 11

ID	MICM_MOUSE	STANDARD;	PRT;	476 AA.
AC	P01873;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DR	Ig mu chain C region membrane-bound form.			
OS	Mus musculus (Mouse);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TAXID=10090;			
RN				
RP	SEQUENCE OF 433-476 FROM N.A.			
RA	MEDLINE=8222874; PubMed=6771020;			
RA	Early P., Rogers J., Davis M., Calame K., Bond M., Wall R.,			
RA	Hood L.;			
RT	"Two mRNA can be produced from a single immunoglobulin mu gene by RT alternative RNA processing pathways.;"			
RL	Cell 20:313-319(1980).			
RN				
RP	SEQUENCE OF 410-476 FROM N.A. (MYELOMA MOPC 104E).			
RA	MEDLINE=80222873; PubMed=6771019;			
RA	Rogers J., Early P., Carter C., Calame K., Bond M., Hood L.,			
RA	Wall R.;			
RT	"Two mRNAs with different 3' ends encode membrane-bound and secreted RT forms of immunoglobulin mu chain.;"			
RL	Cell 20:303-312(1980).			

FT STRAND 122 126 126 /FTId=VAR_003888.

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteraria; Insectivora; Soricidae; Crocidurinae; Suncus.

OC NCBI_TaxID=9378;

OC [11]_TaxID=9378;

OC RN

RP

RC

RT

RT TISSUE=Liver;

RX

RA

RA Ishiguro H., Ichihara Y., Namikawa T., Nagatsu T., Kurokawa Y.,

RA "Nucleotide sequence of *Suncus murinus* immunoglobulin mu gene and

RA comparison with mouse and human mu genes.";

RL FEBs Lett. 247:317-322 (1989).

CC

CC MEDLINE=9232144; PubMed=2497033;

CC

Db 344 QLKUREASASITCLVQDFPSPDPVQWQHQGPVDPKRVTSNPTPERQNPQGVFVISLT 403
 Qy 306 VNK31IWEKGQNLVTCRUVHHLRPGSRTLEKSLHYSAG 341
 Db 404 VSKDQWSSGGSFSCUVGHAEALPLSVT-EKAVDXTSG 438

Search completed: February 26, 2004, 11:59:20
 Job time : 19 secs

RESULT 15
 MUC CANFA STANDARD: PRT: 450 AA.

ID MUC CANFA
 AC P01874;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig mu chain C region.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE OF 1-177 (M00).
 RX MEDLINE-80077682; PubMed=117299;
 RX McCumber L.J., Capra J.D.;
 RT "the complete amino-acid sequence of a canine mu chain.";
 RL Mol. Immunol. 16:565-570(1979).
 RP SEQUENCE OF 178-420 (M00).
 RX MEDLINE-78180587; PubMed=5633360;
 RA Wasserman R.L., Capra J.D.;
 RT "Amino acid sequence of the Fc region of a canine immunoglobulin M: interspecies homology for the IgM class.";
 RL Science 200:1159-1161(1978).
 DR PIR: A93131; MHDG.
 DR HSSP: P01857; IFC1.
 DR InterPro; IPR07110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam: PRO0047; Ig_4.
 DR SMART: SM00407; IgG1; 2.
 DR PROSITE: PS50835; Ig_LIKE; 4.
 DR PROSITE: PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 SQ SEQUENCE 450 AA; 48895 MW; 9D460D49D1012F5D CRC64;

Query Match 23.9%; Score 444; DB 1; Length 450;
 Best local similarity 32.3%; Pred. No. 7.6e-27;
 Matches 111; Conservative 50; Mismatches 143; Indels 30; Gaps 13;
 Spacers 111;
 Qy 10 LSPE--SGVTLIPTPKVLFHSSCDPGRDAHSTIQLICLVSFRSPAKKHMV-LVQGQE 66
 Db 106 LTLPPBVG--FIPRDAFPG--BPKAS---QLICQASQFSPRQV--WSLRQKQ 151
 Qy 67 AENLFPYTT---RPKRECQTSLOSEVNITQWQNSNTYTCVHKGNSIF-EDSSR 120
 Db 152 IES--GVTTEVVAZAKZSCPTVKTSMITQIOPDAWLSQSVFICKVHRRGLTQONASS 209
 Qy 121 KCADSNPRGSAVSRPSPDPLFRKSPTITCLVQDLPKGQTNLWRSRASCKPVHST 180
 Db 210 MCTSDDPVGISIFTIPPSFASIFNTRSAKSLCLVYDIA-TYDSDVTLISREENGALKHT 268
 Qy 181 RKEEKORNGLTLVISTLIPYDWTMGEYVQCRVTHPLRPLMESTIKLPGRL-APEV 239
 Db 269 NISESHPNGTFSAMGATVVEEWSGEOTCTVTHDLSVQKOTISRPKGVAVHMSV 328
 Qy 240 YMLPSPSPEETG-TTRPTVTLIRGYPSEISVQWLFNPNEDHDHTGHTTRPQDQHGADPS 297
 Db 329 YVLPSPSREQDIRESATLSCLVQYSPDPVYVQWYQSGPPVPPDSYVTSAPMPERQAPGL 388
 Qy 298 FFLYSPMLVNLKSIWEKGQNLVTCRUVHHLRPGSRTLEKSLHYSAG 341
 Db 389 YFAHSILTVSEEWMAGETTTCVVAHESLP-NRVTERSVDKSTG 431

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	CompuGen Ltd.					
OM protein - protein search, using sw model						
Run on:	February 26, 2004, 11:45:31 ; Search time 20 Seconds					
Scoring table:	BL0SUM62					
Searched:	US-09-401-636-8 1856 1 EFPHHHRHTLSPESGVVTI.....HEALPGSRTLKSLSHVSGN 342					
Minimum DB seq length:	0					
Maximum DB seq length:	200000000					
Total number of hits satisfying chosen parameters:	283366					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
Database :	PIR 7B: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5: pir5: 6: pir6: 7: pir7: 8: pir8: 9: pir9: 10: pir10: 11: pir11: 12: pir12: 13: pir13: 14: pir14: 15: pir15: 16: pir16: 17: pir17: 18: pir18: 19: pir19: 20: pir20: 21: pir21: 22: pir22: 23: pir23: 24: pir24: 25: pir25: 26: pir26: 27: pir27: 28: pir28: 29: pir29: 30: pir30: 31: pir31: 32: pir32: 33: pir33: 34: pir34: 35: pir35: 36: pir36: 37: pir37: 38: pir38: 39: pir39: 40: pir40: 41: pir41: 42: pir42: 43: pir43: 44: pir44: 45: pir45:					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result	% Query					
Score	Match Length					
DB ID	Description					
1	1038.5	56.0	428	1	ERHU	Ig epsilon chain C
2	1024.5	55.2	426	1	I16948	Ig epsilon-chain -
3	767.5	41.4	429	1	ERHT	Ig epsilon chain C
4	751	40.5	388	1	ERMS	Ig epsilon chain C
5	682	36.7	548	2	S38864	Ig epsilon chain C
6	673	36.3	423	1	ERMS	Ig epsilon chain C
7	580.5	31.3	572	2	S46529	Ig Y-heavy chain
8	535.5	28.9	504	2	S46529	Ig gamma chain (c1
9	497.5	26.8	479	1	MERBM	Ig mu chain C regi
10	496	26.7	454	1	MERY	Ig mu chain C regi
11	495.5	26.7	454	1	MERY	Ig mu chain C regi
12	486.5	26.2	326	1	G2HUU	Ig mu chain C regi
13	480.5	25.9	343	2	S25644	Ig mu chain C regi
14	476	25.6	327	1	G4HUU	Ig gamma-4 chain C
15	475.5	25.6	627	2	S14683	Ig mu chain precursor
16	473.5	25.5	328	2	I47161	Ig gamma 2a chain
17	472	25.4	433	2	S31436	Ig gamma 3 chain C
18	469	25.3	455	1	M6MS	Ig upbeta chain -
19	469	25.3	455	2	A24976	Ig mu chain C regi
20	469	25.3	476	1	M6MS	Ig mu chain C regi
21	468	25.5	328	2	I47160	Ig gamma 2b chain
22	465	25.1	328	2	I47159	Ig gamma 3 chain C
23	465	25.1	453	2	S37768	Ig mu chain C regi
24	465	25.1	474	2	S15590	Ig heavy chain - h
25	463.5	25.0	328	2	I47158	Ig gamma 1 chain C
26	460	24.8	391	1	M6HUBT	Ig mu heavy chain
27	458.5	24.7	592	2	S35705	Ig mu chain - shee
28	458.5	24.5	1	GRHU	Ig gamma-1 chain C	
29	453.5	24.4	452	1	M6HU	Ig mu chain C regi

A;Residues: 'GAWL', 6, 'X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 124, 'R';Experimental source: myeloma protein Nid R;Kenney, J.T.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; C proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982

A;Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon;Accession: B01933; NID:8306234; PMID:6816656

A;Residues: 1-40; 68:114-427-428 <KEN>

A;Cross-references: GR:100022; NID:9185035

R;Ikeyama, S.

R;BBS Lett. 224, 306-310, 1987

A;Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment R;Reference number: S02438; NID:88083554; PMID:3121387

A;Accession: S02438

A;Status: nucleic acid sequence not shown

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 98-352 <IKE>

R;Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.

R;J. Biol. Chem. 269: 456-462, 1994

A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A;Reference number: A53116; NID:94103254; PMID:8278835

A;Accession: A53116

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 320-428 <ZH2>

A;Experimental source: myeloma U266-derived cell line AF-10

A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIPI:141702)

R;Heilman, L.

R;Bur. J. Immunol. 23, 159-167, 1993

A;Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of A;Reference number: A46536; NID:9122085; PMID:8419166

A;Accession: C46536

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 382-391 <HEB>

A;Cross-references: GB:SS5273; NID:9263166; PIDN:AB24857.1; PID:9263167

A;Experimental source: B cell myeloma U-266

A;Note: sequence extracted from NCBI backbone (NCBIPI:125297)

A;Accession: D46536

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 382-391 <HEB>

A;Cross-references: GB:SS5276; NID:9263168; PIDN:AB24858.1; PID:9263169

A;Experimental source: B cell myeloma U-266

A;Note: sequence extracted from NCBI backbone (NCBIPI:125299)

A;Accession: A46536

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 401-428 <HE3>

A;Cross-references: GB:SS3497; NID:9263162; PIDN:AB24855.1; PID:9263163

A;Experimental source: B cell myeloma U-266

A;Note: sequence extracted from NCBI backbone (NCBIPI:123483)

A;Genetics:

A;Gene: GDI; IgHE

A;Cross-references: GDB:119335; OMIM:147180

A;Map position: 14q32.33-14q32.33

A;Introns: 1/1; 104/1; 211/1; 319/1

A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a C Superfamily: immunoglobulin C region; immunoglobulin homology <IM1>

C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM1>

F;22-87/Domain: immunoglobulin homology <IM1>

F;128-301/Domain: immunoglobulin homology <IM2>

F;232-301/Domain: immunoglobulin homology <IM3>

F;338-407/Domain: immunoglobulin homology <IM4>

F;14-51/Disulfide bond: interchain (to light chain) #status Predicted

F;155-105, 29-85, 135-113, 238-299, 345-405/Disulfide bonds: #status Predicted

F;211-49, 99-146, 252, 215/Binding site: carbohydrate (Asn) (covalent) #status Predicted

F;121-209/Disulfide bonds: interchain (to heavy chain) #status Predicted

Query Match 56.4%; Score 1038.5; -DB 1; Length 428;

Best Local Similarity 62.6%; Pred No. 9-97-71;

Matches	201;	Conservative	41;	Mismatches	73;	Indels	7;	Gaps	4;
QY	22	PPTVKLFHSSCDPGRPAHSITQQLCIVSGESPAKUHNTMVDQBAENLRYPTTRPKRKG	81						
Db	111	PPTVKLQILOSSCDGGGRHFPPTIQLCIVLNSGTYPTGTTNTLFDGQMD-	168	VDLSTAS-TT08					
QY	82	GQTFSQESEVNITQGOMMSNTTICHVKANGSIFEDSRKCADSNPRGVSAYLSRSPFD	141						
Db	169	GHLASTQSELNLISQKWLSDRTYQCTYQHTPDTKCADSNPRGVSAYLSRSPFD	228						
QY	142	LFIKRSKPTITLVLQDPLA5KGCVNLTWSRASGKPVNHSKKEEQLQNLIVTSLPGT	201						
Db	229	LFIKRSKPTITLVLQDPLA5KGCVNLTWSRASGKPVNHSKKEEQLQNLIVTSLPGT	288						
QY	202	RDWIEGTYQCRVTHPHPRALMRSITKPGKRLAPEVNMPLPPSPEETGT--TRTVCLL	259						
Db	289	RWIEGTYQCRVTHPHPRALMRSITKPGKRLAPEVNMPLPPSPEETGT--TRTVCLL	347						
QY	260	RQFYPESTIVSOWLNENPDEDTGHMTRPKDHDGTPSPFLYSLVNUKSIWECNLVTC	319						
Db	348	QNFMPDPDISVOWLHNENVOLPDKRHSITOPRKTGS-GFPVFSRLBVTRABWEOKDEFIC	405						
QY	320	RVYHEILPGERTLIESLHRYAG	341						
Db	406	RAVHEIASPSTQVQRAVSVNPG	427						
RESULT 2									
136948									
IG epsilon-chain - chimpanzee (fragment)									
C;Species: Pan troglodytes (chimpanzee)									
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000									
C;Accession: YI-16948									
R;Sakoyama, Y.; Hong, K.									
proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987									
A;Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangutan									
A;Reference number: 136948; PMID:87147196; PMID:3103123									
A;Accession: IJ6998									
C;Superfamily: immunoglobulin C region; immunoglobulin homology									
F;336-405/Domain: immunoglobulin homology <IMM>									
A;Status: preliminary; translated from GB/EMBL/DDBJ									
A;Residues: 1-426 <RES>									
/Cross-references: GB:1M1398; PMID:9176797; PID:AA335416.1; PMID:9176798									
C;Genetics:									
A;Introns: 103/1; 319/1; 317/1;									
A;Homolog: immunoglobulin C region; immunoglobulin homology									
F;Best Local Similarity 61.7%; Pred. No. 1.1e-69; Indels 7; Gaps 4;									
Matches 198; Conservative 42; Mismatches 23									
Db	83	PTVKLHSSCDPGRDAHSITQQLCIVSGESPAKUHNTMVDQBAENLRYPTTRPKRKG	82						
QY	168	ELASTOSELTSQKWLSDTPTTYCQTYGGTFTDSTTKCADCNSPRGVAYLSRSPFDL	227						
Db	143	FIKSTITCIVDPLA5KGCVNLTWSRASGKPVNHSKKEEQLQNLIVTSLPGT	202						
QY	228	PTVKLQILOSSCDGGGRHFPPTIQLCIVLNSGTYPTGTTNTLFDGQMD--VDLSTAS-TT08	287						
Db	203	DWIEGTYQCRVTHPHPRALMRSITKPGKRLAPEVNMPLPPSPEETGT--TRTVCLL	260						
QY	288	DWIEGTYQCRVTHPHPRALVRSITKSPRAMEVYAF-ATTEPGPSRDKRLLAQ	346						
Db	261	GFYPSLISVOMLFNNEBEDHGHTTRPKDHDGTPSPFLYSLVNUKSIWECNLVTC	320						
QY	347	NMPEDISVQVHLNEVOLPDKRHSITOPRKTGS-GFPVFSRLBVTRABWEOKDEFIC	404						
Db	321	VVHEALPGSRTELEKILHYSAG	341						

Db 405 AVHEAASPSQTVQRTVSVNPG 425

A;Reference number: A02144; MUID:83117774; PMID:6818553
A;Accession: A02144

A;Molecule type: mRNA

RESULT 3
EHRIG epsilon chain C region - rat

Ig epsilon chain (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999

C;Accession: A93442; A99397; A02143

R;Heilmann, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.

Nucleic Acids Res. 10, 6041-6049, 1982

A;Title: Structure and evolution of the heavy chain from rat immunoglobulin E.

A;Reference number: A93442; MUID:83064537; PMID:6292865

A;Molecule type: mRNA

A;Residues: 1-429 <HEL>

A;Experimental source: strain LOUc/Wb1, immunocytoma IR2

R;Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.

DNA 1, 335-343, 1982

A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, i

A;Contents: myeloma IR152

A;Accession: A9037

A;Molecule type: mRNA

A;Residues: 'N', 163-307 'L', 309-342 <KIN>

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) chains disulfide bonded. In some cases, such as IgA and IgM, the subunits associate into 1a

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;1-44:Domain: immunoglobulin homology <IM2>

F;1-18-80:Domain: immunoglobulin homology <IM3>

F;18-18-186:Domain: immunoglobulin homology <IM2>

F;21-27-291:Domain: immunoglobulin homology <IM4>

F;327-398:Domain: immunoglobulin homology <IM4>

F;46-99-170, 240, 265, 369-419:Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Similarity 40.5%; Score 751; DB 1; Length 388;

Best Local Similarity 44.8%; Pred. No. 4e-49; Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;

Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 4;

Db 17 PVTIIPPTVKLFHSSCDPRAHDTIQLQILGVSGSPAKVHVTWLVDGOBAENLFPYTR 76

Db 97 PWNITKPTVOLHSSCDPNA-FHSPTIQLCPFVGHQIQLVNDVSHMLNDRIK----YETH 150

Db 77 PK---REGQTFSLQSEVNITQGOMMSNTYCHVKGNSIFEDSSRKADSNPRGVA 132

Db 151 AQNVLIKEEKGLASTYRSRNIQDQWMSSESTPCKVTSQENTWAHTRRCSDDPDEPGVIT 210

Db 133 YLRSRSPFDIFRKSPPTICLWVLDAPSQKPTNHSRKKEKORGILT 192

Db 211 YLIPPSPLDLYENGKPLKTLVLDI-ESSENITYWVREKKIGSASQRSTKHNAT 269

Db 193 VTSIPVPGTGDWIKERTYQCRVTHPLPMLRMSITKPGKRLAPELLMLPPSPPEETGTT 252

Db 270 ITSLIPDVAKWDTGEGYQCRVHDHPKPKIVSRSTKAGKRSAPAVTFLPPEEEKDK 329

Db 253 RVTGCLRGYPSSESVQMFNEERDHTGHTTRPQDQGTDPSFLYSLVNLVKTWE 312

Db 330 RLTLCQIQNTPEDISVQMLQDKLIPKQSHSTPLKQNGSNQFIFSRLEVTKALWT 389

Db 313 KGNLVIQTVRVLHALPSRTKLSKLYSAGN 342

Db 390 QTKQFICRVLHEALRPRKERTISKGN 419

RESULT 4

EMMS Ig epsilon chain C region (version 1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C;Accession: S8864

R;Kipp, B.; Becker, W.; Schlaak, M.

Submitted to the EMBL Data Bank, November 1993

A;Description: Combination of a defined specificity and desired isotype by cloning of an

A;Reference number: S8864

A;Accession: S8864

A;Molecule type: mRNA

A;Residues: 1-548 <KIN>

A;Cross-references: EMBL:227397; PID:9416537; PRDN:CAA81788_1; PID:9440782

C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM2>

C;Cross-references: EMBL:227397; PID:9416537; PRDN:CAA81788_1; PID:9440782

Best Local Similarity 36.7%; Score 682; DB 2; Length 548;

Matches 142; Conservative 52; Mismatches 122; Indels 14; Gaps 4;

Db 12 LPESGVWILPPPTVKLFHSSCDPRAHDTIQLQILGVSGSPAKVHVTWLVDQGAE 69

Db 229 VPEVSVFIPPKP-----DVLTRSTQIYCFYHTINDVSYWMLNDRE 278

Db 70 LFPYTTPKREGQGTFSLQSEVNITQGOMMSNTYCHVKGNSIFEDSSRKADSNPRG 129

A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.

Matches	118; Conservative	56; Mismatches	137; Indels	25; Gaps	10;
Qy	17 PTYIIPPTVKLH--SSCDPREGDAHSTIQTLCLVSGSPAKVHVTMNDGSGEAENLFPYT	75			
Db	172 PVPVPAPEVQVHLHASCTP---SOSSEVELLCLVTGSPASADEVNLVDG--VGGILVASQ	227			
Qy	76 RPKREGQQTFSQSEENITQGOMMSNTYCHVKGH--NGSFEDSSRKADS---NPRG	129			
Db	228 SPAVRGSGTYSQSSRVSRYVNTDREGSKSYSSVRHATNTWEDWKGCPDGQSCSP--	285			
Qy	130 VSAYLSPSPFDLFIKSPTTCLVVLAPSKGTNLITWSRASGKVNHSKTRKEKQNG	189			
Db	345 TYSASASPVNSTDWMSGERFCTVQHEELPLPLSISVYRNTGPTTPLLIPFAPHPPEEL	404			
Qy	190 TLTVTSTLIPVGTRDWMEGETYQCRVTHPLRMLMSTTCKLPGKLAPEVYMLPSSPEET	249			
Db	465 SKMSVETAKWNGGTVFACMVAHEALPHMFSORTLQK	500			
RESULT 9					
MHRBM	IG mu chain C region, membrane-bound form - rabbit				
C;Species	Oryctolagus cuniculus (domestic rabbit)				
C;Date	04-Dec-1986 #sequence_revision 30-Jun-1991 #text_change 23-Aug-1997				
C;Accession	A02165; A02164				
J;Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.					
A;Title	Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of v-Ha2 a				
A;Reference number	A02164; MUID:84088930; PMID:6418803				
A;Contents	a2 allotpe				
A;Accession	A02165				
A;Residues	439-479 <BE2>				
A;Accession	A02164				
A;Residues	439-479 <BE2>				
A;Molecule type	mRNA				
A;Residues	1-438				
A;Note	the sequence of residues 1-438 was assumed to be identical with the corresponding C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a				
C;Superfamily	immunoglobulin C region; immunoglobulin homology				
C;Keywords	alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobulin F,128-200/Domain: immunoglobulin homology <IMM1>				
F,128-200/Domain: immunoglobulin homology <IMM2>					
F,238-306/Domain: immunoglobulin homology <IMM3>					
F,345-416/Domain: immunoglobulin homology <IMM4>					
F,45-112-139-192-210-238-217-280-326-441/Binding site: carbohydrate (Asn) (covalent) #s					
F,21-97/Domain: immunoglobulin homology <IMM1>					
F,130-202/Domain: immunoglobulin homology <IMM2>					
F,242-310/Domain: immunoglobulin homology <IMM3>					
F,349-420/Domain: immunoglobulin homology <IMM4>					
F,44-139/99/Domain: carboxy-terminal <CTS>					
F,28-50,137-200,249-308,356-418/Disulfide bonds: #status predicted					
F,46,114,212,261,271,277,284/Binding site: carbohydrate (Asn) (covalent) #status predicted					
F,219/Disulfide bonds: interchain (to heavy chain) #status predicted					
F,296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted					
Query Match	26.7%; Score 497.5; DB 1; Length 479;				
Best Local Similarity	32.9%; Pred. No. 6, 4e-30;				
Matches	117; Conservative 61; Mismatches 153; Indels 25; Gaps 10;				
Qy	5 HHHHTLSPESGAV-TIIPPTVKLHSSCDPR---GDAHSTIQTLCLVSGSPAKVHVT	59			
Db	94 HSNNSNDRIVPSFVDDSELPNNPSV--IPPDSDFSGSGTGRSKRSLQATGSPQKIVS	150			
Qy	60 WLTQDQEAN--LPPVTPKREGGTSLOSENVITQGOMMSNTYCHVKGNSIFE	116			
Db	151 WLRDGQKVESVLTQPKVPAETKGAGPAPTSISMLTITESDWLQSLYTCRDHRGIFED	210			
Qy	117 DS--SRKCADSHPRGVISYLSRSPSPFDLFIKSPTTCLVVLAPSKGTNLITWSRASG	173			
RESULT 10					
MHY	IG mu chain C region - golden hamster				
C;Species	Macacus rhesus (golden hamster)				
C;Date	30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996				
C;Accession	A02168				
R;McGuire, K.L.; Duncan, W.R.; Tucker, P.W.					
Nucleic Acids Res. 13, 561-5628, 1985					
A;Title	Phylogenetic conservation of immunoglobulin heavy chains: direct comparison of				
A;Reference number	A02168; MUID:85297761; PMID:2594005				
A;Accession	A02168				
A;Molecule type	DNA				
A;Residues	1-454 <MCG>				
A;Note	the sequence was determined from the germline gene				
A;Note	the authors translated the codon GST for residues 105 and 324 as Val and Glu respectively				
C;Genetics					
A;Intron	105/3, 218/3; 324/3				
C;Complex	An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a				
C;Superfamily	immunoglobulin C region; immunoglobulin homology				
C;Keywords	duplication; glycoprotein; heterotrimer; immunoglobulin F,128-200/Domain: immunoglobulin homology <IMM1>				
F,128-200/Domain: immunoglobulin homology <IMM2>					
F,238-306/Domain: immunoglobulin homology <IMM3>					
F,345-416/Domain: immunoglobulin homology <IMM4>					
F,45-112-139-192-210-238-217-280-326-441/Binding site: carbohydrate (Asn) (covalent) #s					
F,135-198,245-304,352-414/Disulfide bonds: #status predicted					
Query Match	26.7%; Score 496; DB 1; Length 454;				
Best Local Similarity	34.5%; Pred. No. 7, 8e-30;				
Matches	119; Conservative 60; Mismatches 150; Indels 16; Gaps 9;				
Qy	5 HHHHTLSPESGAV-TIIPPTVKLHSSCDPR---GDAHSTIQTLCLVSGSPAKVHVT	60			
Db	91 HHHHTNKKDVKLVRVPIG-VTEMNPNTVSVPVSDAFSPGPKRSRFLCERASNSFSPKQITWS	149			
Qy	61 LDVGDQAENLF--PITPRKREGGQPSLQSOBVNTQGOMMSNTYCHVKGNSIFE	116			
Db	150 LDDQPKVSGFTTTPVPTEDRSGSPRKTIVTSLITDWNLTSVTCYDHRGLTFW	209			
Qy	117 DSSRKCADSNPRGVISYLSRSPSPFDLFIKSPTTCLVVLAPSKGTNLITWSRASGPV	176			
Db	210 NVSATCAASPTIQAFFPSPVGLFLNSKSLTICVNTLA-TYPTLNISSSRSGEPL	268			
Qy	177 NHSTRKKEKQNRNMLTVTSTLPGTROMIEGYYQCRVTHPLRMLRSTTRKLP-KRL	235			
Db	269 ETKTKLGETSHPNQTSATGAVNQCVEDWDSKGEFKVCTWHDLPSQKFKLSPKRGAKT	328			
Qy	236 APETYMLPPSPES--TGTRTVCILRGYPYRBSISVOWLFNNEEDHTGHHTTRPDKHDG	293			
Db	329 PPAVYQOQPLAREMILRESEATVTCVKGKSPADIFVOMLQRGQLPSQDQKIVTSSAPREPO	388			
Qy	294 TDSPPFLYSSRMLNKSMEWKGNTVCVYHEALP--GSRTLEK	335			
Db	389 APLHYPTVSLVTTBEEWNSGETYTCVVGHEALPHMVTERTVDS	433			

RESULT 11

MRB

Ig mu chain C region, secreted form - rabbit

C.Species: Oryctolagus cuniculus (domestic rabbit)

C.ID: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 23-Aug-1997

CACcession: A02164

A;Residue: K-E; Alexander, C.B.; Reddy, E.P.; Mage, R.G.

J. Immunol. 132, 490-495, 1984

A;Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of v-Ha2 a

A;Contents: a2 allotype

A;Accession: A02164

A;Molecule type: mRNA

A;Residues: 1-458 **BPF**

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu

l;R:130-202/Domain: immunoglobulin homology <IM1>

F:242-310/Domain: immunoglobulin homology <IM3>

F:749-920/Domain: immunoglobulin homology <IM4>

F:14/Disulfide bonds: interchain (to light chain) #status predicted

F:28-90,137-200,356-418/Disulfide bonds: #status predicted

F:46,114,212-261,277,284,415/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:219,457/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

F:296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 26.7%; Score 495.5; DB 1; Length 458;

Best Local Similarity 33.1%; Pred. No. 8.6e-30; Matches 116; Conservative 61; Mismatches 148; Indels 25; Gaps 10;

QY 5 HHHHTLSPESGV-TIIPPTVLPKFLHSSCDPR---GDAHSTIQLICLVSFGSPARVHT 59

Db 94 HSNNSRDLRVSFPVDSLPELPNVSF--IPPRDSFGSGTRKSRLICQATGFSPKQISVS 150

QY 60 WLDQGQABRN--LFPYVTPRKEGGQFQFSQSEVNTOGQWMSNVYTCKWKS1F8 116

Db 151 WLRDGQKVBESGVTKPVEATKQGAPATFISISSLMTTESDWLISOLSYTCRDVHGGFF 210

QY 117 DS--SRKCADSPRGRGSAVLSRSPDPLIRKSPITCIVLDAASKGIVNLNTSRASG 173

Db 211 KNYMSMSSBCTTSPGIVOPPIAIFADTFLSKSARLICLVLNDT-TYGSNLNTWASHNG 269

QY 174 KPNWHSRTRKEKORNGITIVTISTLPGIRDMEGETVQCRVTHPFLRAMLSTIKLPGK 233

Db 270 KAHDTHMNNTESHPNATPSAMGASVCAEDWESGEQDTCVTHADPPLKHTSK--SR 327

QY 234 RLA--PEVYMLPPSPPEB--TGTRTVVILQIYRYPBSVIVWLPNRRBDRNGHTTRP 288

Db 323 EVAKHPVAVVLPKAREQVLRSATVIVLKGSPADVFVWQDQGQPLSSDKVTSAP 387

QY 289 OKDQGTDSPFLPFLYSLRMLYNTISWKGKNTVCRVHEALP--GSRTELEKS 335

Db 388 APERQAPGIVKTFITLIVTIEBEDWNSGETTCVGHERALPHMVTERTVDS 437

RESULT 12

G2HU Ig gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000

C;Accession: A93906; A02809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con

A;Reference number: A93906; MUID:82197621; PMID:6801948

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-326 <ELL>

A;Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CA858438.1; PID:96056056

A;Note: Lys-26 is probably removed posttranslationally

R;Huang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and

A;Reference number: A92809; MUID:8107873; PMID:6774012

A;Contents: myeloma protein T11

A;Accession: A92809

A;Molecule type: protein

A;Residues: 1-19 'Q' 21-57 'Z' 59 'A' 61-193 'D' 195-325 <MAN>

A;Note: Trp-156 is at or near the complement-binding site

R;Connelly, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A;Title: The amino acid sequences of the three heavy chain constant region domains of a

A;Reference number: A90752; MUID:80001357; PMID:113060

A;Contents: myeloma protein Z11

A;Accession: A90752

A;Molecule type: protein

A;Residues: 1-24 'E' 26-57 'EV' 60-85,132-171 'ZZZ' 175 'B' 177-193, 'D' 195-196, 'Q' 198

A;Note: this sequence has since been revised

R;Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A;Reference number: A93132; MUID:80114419; PMID:118920

A;Contents: Z11

A;Accession: A93132

A;Molecule type: protein

A;Residues: 238-275 <EOF>

R;Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A;Contents: annotation; Z11, revisions to residues 25, 59, 60, and 264-268

A;Reference number: A94591

A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat

ned

R;Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A;Reference number: A90253; MUID:7203350; PMID:490472

A;Contents: annotation; myeloma protein Sa, disulfide bonds

R;Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A;Title: Structural studies of immunoglobulin G.

A;Contents: annotation; Sa, disulfide bonds

C;Genetics:

A;Gene: GDB:IGR2

A;Cross-references: GDB:119338; OMIM:147110

A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:221-251/Domain: immunoglobulin homology <IM1>

F:234-264/Domain: immunoglobulin homology <IM2>

F:274-304/Domain: immunoglobulin homology <IM3>

F:299-306/Domain: immunoglobulin homology <IM4>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:212-231/140-260,246-304/Disulfide bonds: interchain (to heavy chain) #status experimental

F:102,103,105,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.2%; Score 486.5; DB 1; Length 326;

Best Local Similarity 36.2%; Pred. No. 2.7e-29; Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGDASHSTIQLICLVSFGSPARVHTW--JVDQGELENFLYTRIKRKGCGCTPSQSE 90

Db 16 RSTSTAAAGLCLVYKTDVPPPTVWPSWNGALSTG--VHTPAVL---QSGLYLSSV 68

QY 91 VNIUTQGOMMSNTVTCVKG--NGSFEDSSRKCAASNP----RGVSIYLSPSPF 140

Db 69 VTVPSNSP-GTQTYTCVNTDVKPNTKVKVTKCCTVCCPFPAPPVAGPSVFLFPKPK 127

QY 141 D-LFIRKSTITLCLVVDLAPSKGTVNTLWSRASKGPKVHNSTRKGKRGNTITVSTLPU 199

Db 128 DTLMISRTPEVTCVWVPSHEDPVQFWVYQVEMAKTPREQFNSTFRVSVLTV 187

RESULT 13
 S25644 Ig mu chain C region - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 21-Jan-2000
 C;Accession: S25644
 R;Parker, K.; Bioger, L.; Souillou, J.-P.
 submitted to the EMBL Data Library, September 1992
 A;Reference number: S25644
 A;Accession: S25644
 A;Molecule type: mRNA
 A;Residues: 1-343 <PAR>
 A;Cross-references: EMBL:X69312; NID:956461; PIDN:CAA48392.1; PID:9818025
 A;Experimental source: spleen
 C;Genetics:
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;234-305/Domain: immunoglobulin homology <IMM>
 Query Match 25.9%; Score 480.5; DB 2; Length 343;
 Best Local Similarity 34.7%; Pred. No. 82-29; Mismatches 108; Conservative 59; Indels 13; Gaps 7;
 Matches 108; Conservative 59; Mismatches 131; Indels 13; Gaps 7;
 Query 36 GDAHSTIQQLCLVSGFSPAKVHVTWLGQAEANLFR--PYTRPRKGGSQFSLOSEVN 92
 Db 14 GPKPRSKRSLICEATNFSPKQITVSWLQDGPKVSGFTEPVTVEAKSRPQTYKVSLT 73
 Query 93 ITRQGQWMSNTYCHVKGNSIF-EDSRKCADSNPRGVASVLSRSRSPFDIFIRSPIT 151
 Db 74 IATSDWNLNVFTCRVDRGLTQWVNSTCAASPDILAPPPIPSFADIFLTAKLS 133
 Query 152 CUVVLDLAPSKGTKTNTLWSRASKGPKVHNSTRKEKQRTGILTVTSPVIGRDWIEGTYQ 211
 Db 134 CLVNTNL-A-TYDTUNIHSNSKSCBPLBNTKTMESHGNGT-RAVGWASVCMEDWDNRKEFV 192
 Query 212 CRYTHPHILPRLMRSTTKLPGK--R-LAPEVYMLPPSPRE-TGTTTGTCTLGRGPSEI 267
 Db 193 CTWTHRDLPSPQKETISK-PNEVAKHPPAVWLLPAREQLIRESATVTCVKGFSFADI 251
 Query 268 SWVQLFNEEDHHTHTPDKDGTDPSPFLYSLRMLVNUKSIWELKGNTVCRVHEALP 327
 Db 252 FVQWLQRCQPLSSDDKYVVISAPMPEPPGAGLYFTHSILTVSEWNSGETYTCVVGHALP 311
 Query 328 ---GSRLEKSL 335
 Db 312 HMVTERTVDKS 322
 RESULT 14
 S14633 Ig mu chain precursor, membrane-bound (clone 201) - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
 C;Accession: S14633; S08047
 R;Friedlander, R.M.; Nusseineig, M.C.; Leder, P.
 Nucleic Acids Res. 18: 427, 1990
 A;Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain
 A;Reference number: S14633; MUID:9032450; PMID:2115996
 A;Accession: A90933
 R;Ellison, J.; Binkbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A;Reference number: A90933; MUID:83157104; PMID:6299662
 A;Accession: A90933
 G4HU Ig gamma-4 chain C region - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
 C;Accession: A90933; A90249; A0150
 R;Ellison, J.; Binkbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A;Reference number: A90933; MUID:83157104; PMID:6299662
 A;Accession: A90933
 A;Cross-references: EMBL:X17115; NID:933450; PIDN:CAA34971.1; PID:933451
 A;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin; membrane protein

F;1-15/Domain: signal sequence #status predicted <SIG>
 F;16-627/Product: Ig mu chain #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology

Query Match 25.6%; Score 475.5; DB 2; Length 627;
 Best Local Similarity 31.4%; Pred. No. 4.1e-28; Mismatches 142; Indels 25; Gaps 10;
 Matches 106; Conservative 65; Mismatches 142; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVLFHSSCDR---GDAHSTHQLICLVLGFSRPAKRYVTLWQGELEN 69
 Db 254 PLPVIAELPPKVSVF--VPPPRDGFFGNPPSKSKLICOATGFSPRQIOVSWLREKGQVGS 310

Qy 70 LFPYTT---RPKREGQGTESLOSEVNTQGOMMSNTYTCVKGNSIF-EDSSRKCA 123
 Db 311 --GVTTDQVQARAKESGPTVYKVTSITIKESDWLQSOMTICRVUDHGLTFQONASMCV 368

Qy 124 DSNPRGVSAYLSRSPFDLFLRKSPITCIVDYLAPSKGNTLMSRASGGKPYWHSTKE 183

Db 369 PDDDTAIRVFAIPPSFASIFLTKSTKLTCVTDLT-YDPSVITSMTRONGEAVKHTNS 427

Qy 184 EKQRNGILTVTSLPVGTRDMEGETQCRTHPILPRLMRSTIKLPGRL-APEVML 242

Db 428 ESHPNATPSAVGEASCTEDDMSNGERFTCTVTHPLSPSKOTISRPKVALHRPDVLL 487

Qy 243 PPSPEETG--TTRIVTOLIRGYPSEISVOMLFNNEEDHTGHHTTRPQDKHGTDPSPFL 300

Db 488 PPAREQINTRSATITOLVIGPSADYFVQMMQRCQPLSEKYYTISAPHEPEPQAPGRFA 547

Qy 301 YSRMLVYKSTWKGNYVTCRVHEALPG--SRTLAKS 335

Db 548 HSILTVSEEWVNTGERTVTCVVAHEALPNRVTERTVDKS 585

Search completed: February 26, 2004, 11:59:54
 Job time : 22 secs